



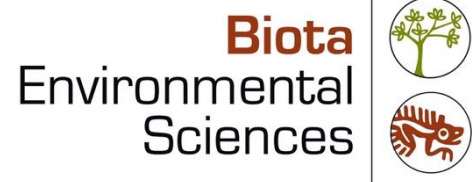
Winu Project SRE Invertebrate Fauna Assessment



Prepared for

Rio Tinto Winu Pty Ltd

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ABN 49 092 687 119
Level 4, 46 Colin Street
West Perth, Western Australia 6005
Ph: (08) 9328 1900

Project No.: 1716G

Prepared by: N. Watson
H. Newton

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Winu Project SRE Invertebrate Fauna Assessment

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1.0 Executive Summary

Rio Tinto Winu Pty Limited plans to develop a new copper-gold mine, referred to as the Winu Project, approximately 320 km east of Port Hedland in the Pilbara region of Western Australia, within both the Nyangumarta and Martu Peoples' Native Title Determination Areas. Considerable biological survey work has been completed to support the environmental impact assessment of the proposal, including the assessment of short-range endemic (SRE) invertebrate fauna in relation to the proposal. This report details all terrestrial SRE invertebrate fauna work undertaken for the Winu Project.

Survey effort targeting SRE invertebrate fauna within the Winu Development Envelope (DE) comprises a total of seven survey phases conducted between August 2017 and May 2024 undertaken for both the Winu Project and the Australian Renewable Energy Hub (AREH). SRE invertebrate fauna was surveyed using two approaches:

1. targeted searches undertaken during detailed and targeted terrestrial fauna surveys; and
2. systematic pitfall trapping during detailed vertebrate fauna surveys, when invertebrate specimens were captured as bycatch.

The total SRE survey effort expended across the Winu and AREH projects amounts to 62 targeted SRE search sites and 68 pitfall trapping sites. The SRE survey effort undertaken specifically within the Winu DE amounts to a total of 38 pitfall sites and 19 targeted SRE search sites. Over 96 person hours were spent on SRE fauna searches across both projects combined, and 32 of these person hours were spent searching within the DE.

A total of 18 putative mygalomorph spider species and five scorpion taxa were recorded (excluding taxa not identified to genus level). All of the 18 mygalomorph spider species are undescribed molecular species. Three of the 18 species have been recorded over 240 km away and are therefore considered unlikely to be SREs. Nine of the remaining 15 taxa have only been recorded within the Winu DE, and all were recorded from only one site. With the lack of additional records for these taxa, they are conservatively assessed as representing potential SRE fauna. All nine taxa were recorded from Shrub and spinifex on sandplain (eight species) and Inland sand dune (one species) habitats, which do not represent restricted or isolated habitats and are contiguous with the same habitats in the wider locality. Two of the five potential SRE scorpion taxa recorded are potential SREs, but both have been recorded outside of the Winu DE. Both taxa were recorded from Inland sand dune habitat.

Five fauna habitats were identified within the DE (plus disturbed/cleared areas). The majority of the DE is represented by Shrub and spinifex on sandplain (72%) followed by Inland sand dune (13%), and Gravelly lateritic rises (13%). Ephemeral claypans, Clayey sandplains with termitaria, and Disturbed/cleared areas make up the remaining portions, each representing less than 1% of the DE.

Of the 15 putative mygalomorph spider species identified as potential SRE taxa, 12 belong to the family Anamidae, a family which dominates in the sandier substrates of the arid zone. The likelihood of the species recorded from the RAC and MIA being restricted in distribution to very small areas like the DE is considered low, since the majority of the habitats identified often lack suitable microhabitats and occur as large, contiguous extents across the wider landscape. It follows that it is highly unlikely that any of these species would be restricted to

the DE and that further survey work would likely extend the known distributions of these species outside of the DE.

East of the MIA, three other mygalomorph families were recorded. Field observations suggest this likely coincides with the higher clay content of the soils in that area, which may represent a habitat isolate and have a higher likelihood of supporting true SRE fauna than the rest of the DE. This unit overlaps less than 1% of the DE and extends outside of the DE south of the project's Rimfire borefield pipeline corridor.

2.0 Introduction

2.1 Project Background

Rio Tinto Winu Pty Limited (RTW) plans to develop a new copper-gold mine, referred to as the Winu Project, approximately 320 km east of Port Hedland in the Pilbara region of Western Australia, within both the Nyangumarta and Martu Peoples' Native Title Determination Areas.

Considerable biological survey work has been completed to support the environmental impact assessment (EIA) of the proposal. Part of this work has been the assessment of short-range endemic (SRE) invertebrate fauna in relation to the proposal. This report details all terrestrial SRE invertebrate fauna work undertaken for the Winu Project. Key terminology for the Winu Project is defined in Table 2.1 and the location of the Winu Project is presented in Figure 2.1.

Table 2.1: Key terminology for the Winu Project.

Term	Definition
The Project	Includes the development of a new below-water table copper-silver-gold deposit and associated infrastructure and activities required to access, process and transport ore.
Development Envelope (DE)	Refers to the combined areas of the mine and infrastructure area, access road and the regional borefield, Rimfire. All activities will occur within this area.
Mine and Infrastructure Area (MIA)	Refers to the area containing the mineralised deposit and related infrastructure. This is the Winu mine site.
Road Access Corridor (RAC)	Refers to the Access Road, which encompasses the entire length of the existing Access Road from Great Northern Highway to the Winu Project Area.
Rimfire Borefield (Rimfire)	Refers to the regional borefield located at Rimfire, which is approximately 31 km from the MIA.

2.2 Spatial Scope of this Report

Multiple fauna surveys targeting SRE invertebrate fauna have been conducted within the Winu DE for the purposes of EIA undertaken for both the Winu Project and the Australian Renewable Energy Hub (AREH). Spatially these two projects overlap, with the RAC intersecting the AREH study area (see Figure 2.1). While the focus of the current scope is on the Winu DE, sampling effort and recorded specimens from outside the Winu DE (but within the AREH study area) as shown in Figure 2.1, are also discussed, as they provide regional context and reference data for the work completed within the Winu DE.

2.3 Study Objectives

The specific objectives of this study were to consolidate and integrate all terrestrial SRE invertebrate fauna work undertaken for the Winu Project into a report consistent with the framework of the proposal referral. Specifically, this comprised:

- consolidating and summarising all supporting surveys undertaken for the Winu Project and their compliance with relevant policy;
- vetting and auditing all invertebrate SRE fauna data into a single master data set (including any updates to taxonomy or conservation status); and
- generating a consolidated account of all records of potential SREs across the DE.

The report was undertaken with reference to the following EPA guidance:

- *Technical Guidance: Sampling of short range endemic invertebrate fauna* (EPA 2016).

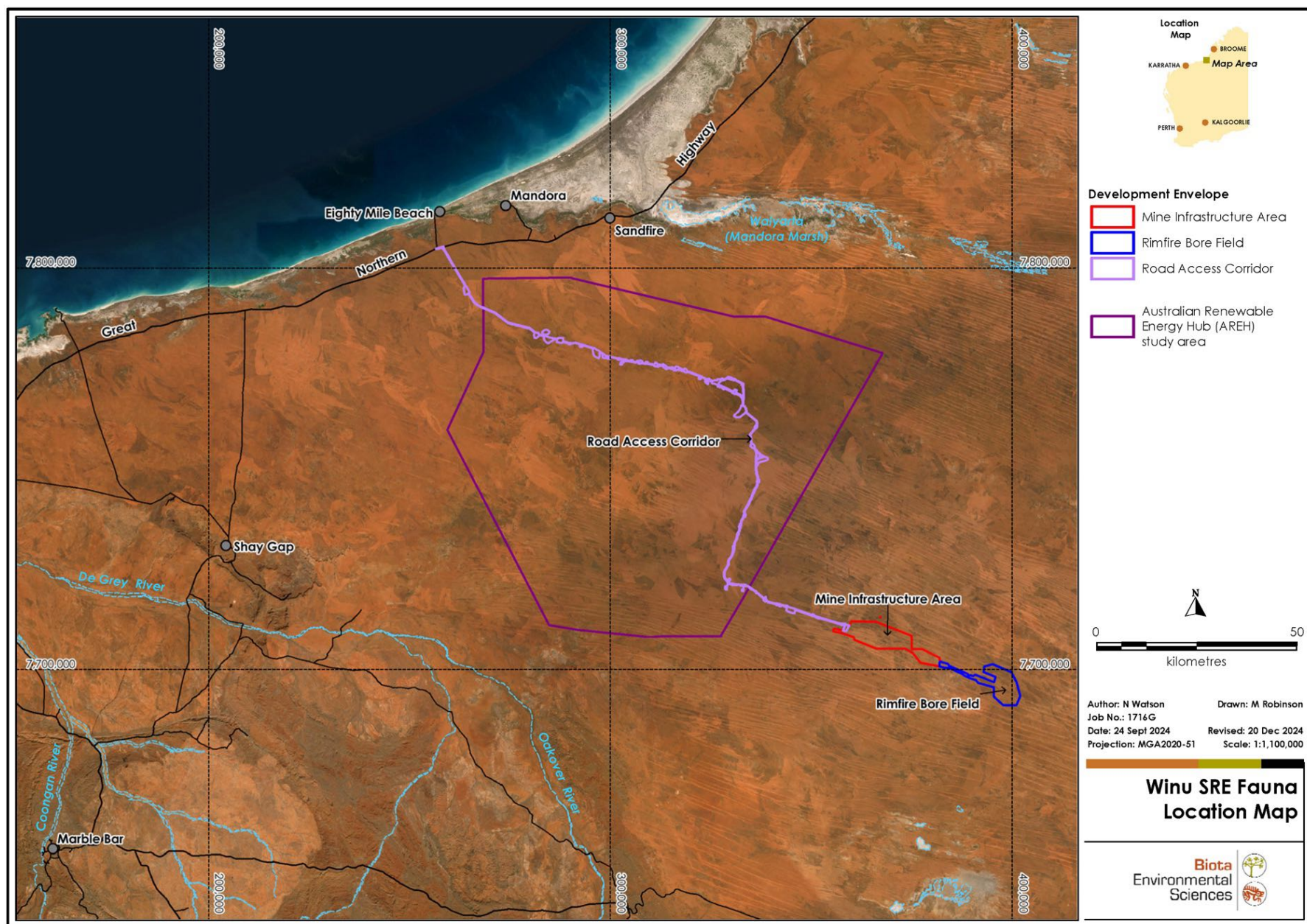


Figure 2.1: Project location and DE.

3.0 Methodology

3.1 Desktop Study

The data consolidated in this report were collated from multiple studies undertaken for the purposes of the Winu Project, and for other studies in the locality which are considered relevant to the project, particularly AREH. Biota holds a large proportion of the biological data, having completed all the fauna surveys to date for both projects over multiple phases.

Desktop studies were completed prior to each project and/or field survey mobilisation, and comprised: literature reviews, database searches and a review of likely SRE habitats and likely SRE groups. The consolidation exercise undertaken in this report reviewed the desktop studies from the source reports and undertook new database searches in order to ensure inclusion of all the latest information (Sections 3.1.1 and 3.1.2).

3.1.1 Literature Review and Database Searches

A range of published and unpublished reports were reviewed to consolidate data from multiple phases. Key studies included:

- Asian Renewable Energy Hub Fauna Survey (Biota 2018);
- Asian Renewable Hub Detailed Fauna Assessment (Biota 2022);
- Winu Project Fauna Assessment (Biota 2021);
- Detailed Flora and Vegetation Mapping of the Winu Project (Interim Vegetation Mapping) (Western Botanical 2024); and
- Landforms Assessment – Winu Project (SLR Consulting 2024).

The following databases searches were conducted using buffers ranging from 40 km to 120 km around a central point in the respective survey area. Queried databases comprised:

1. The *Environment Protection and Biodiversity Conservation Act 1999* (EPBC Act) Protected Matters Search Tool database. This database includes species and communities considered to be Matters of National Environmental Significance (MNES).
2. The Atlas of Living Australia (ALA) database (<http://www.ala.org.au>): a joint project between academic collecting institutions, private individual collectors and community groups. The atlas contains occurrence records, environmental data, images and the conservation status of species throughout Australia.
3. Biota's internal database of SRE records from surveys in the locality.
4. The Department of Biodiversity, Conservation and Attractions (DBCA) NatureMap database. This database was the most comprehensive source of information on the distribution of Western Australia's fauna, comprising records from the Fauna Survey Returns Database and WA Threatened Fauna database (both of the DBCA), and the WA Museum specimen database. It has now been decommissioned.

3.1.2 Review of Habitats and Likely SRE Fauna

The desktop study of likely SRE fauna habitat within the survey area was undertaken using available imagery and contour mapping, taking into account available spatial data, literature and database search results (Section 3.1.1).

As the source surveys consolidated in this report were completed in varying spatial settings and by differing field teams and lead report authors, terminology in describing the habitat units of the DE also varied somewhat from report to report. This is a not uncommon situation that arises with repeated survey effort in the same locality over time whereby what is effectively the same habitat type is described by a slightly different name in different reports. The terrestrial fauna habitats were rationalised into a consistent framework by Biota (2025), which is also followed here. Following EPA (2016), these habitats within the survey area were reviewed considering characteristics with the potential to support SREs, including:

- landforms that represent potential dispersal barriers and could result in the division of populations or cause a reduction in extent of relictual habitats (e.g. boulder piles, isolated hills);
- landforms likely to support specific mygalomorph spider groups (i.e. those in which deep soil profiles with suitable clay content can develop), such as broad valleys with deep loams;
- sheltered habitats and microhabitats likely to support SRE fauna such as land snails and millipedes (e.g. south and east-facing ridges, deep gullies and gorges, and large boulder aggregations, mature spinifex-lined drainage banks);
- isolated habitats; and
- particular vegetation types where vegetation can create microhabitats conducive to SREs (e.g. those likely to produce deep leaf litter).

Sampling site selection was based on the results of the desktop studies prior to the surveys and ground-truthed in the field during the surveys.

3.2 Assessment of Short-range Endemism

SRE invertebrate fauna are invertebrates that exhibit naturally small distributions (less than 10,000 km², per Harvey 2002). Certain taxonomic groups are pre-disposed to short-range endemism as a result of poor dispersal capabilities, confinement to disjunct habitats, slow reproduction and low fecundity (Harvey 2002, Ponder and Colgan 2002). These life-history strategies render these groups vulnerable to localised extinction by relatively small-scale developments, such as mining and construction. Taxonomic groups that show high levels of short-range endemism include mygalomorph spiders, millipedes, pseudoscorpions, and both freshwater and terrestrial molluscs (EPA 2016). Given the importance of short-range endemism to the conservation of biodiversity (EPA 2016), the assessment of such invertebrate taxa is an important component of impact assessment.

The ability to determine whether potential SRE species are actual SREs is limited by knowledge of their biology, distribution and phylogeography, which are in many cases, poorly understood. The taxonomy of SRE invertebrates is patchy and incomplete, which makes determining the conservation significance of potential SRE taxa difficult. To determine the SRE status of putative species recorded from the survey, a range of criteria were used based on the current level of knowledge for each taxon (Table 3.1).

Table 3.1: Criteria used to determine SRE status.

SRE Status	Defining Criteria
Known SRE	- Species, morphotype or genetic type has a documented distribution of <10,000 km². - Species, morphotype or genetic type is well collected with numerous specimens typed and habitat preference understood.
Potential SRE	- Species, morphotype or genetic type has a documented distribution of <10,000 km² but is poorly sampled. - Specimen may not be formally described or assigned to a morphotype / genetic type. - Short-range endemism may be common in genus or family. - May have been collected from restricted, refugia or isolated habitats.
Unlikely to be an SRE	- Species, morphotype or genetic type has a documented distribution of <10,000 km² but is poorly sampled. - Specimen may not be formally described or assigned to a morphotype / genetic type. - Short-range endemism is not common in genus or family. - Taxon was not collected from restricted, refugia or isolated habitats. - Few other individuals of the taxon collected, but records are separated by long distances (>100 km).
Not an SRE	- Specimen formally described or assigned to a morphotype / genetic type. - Species, morphotype or genetic type has a documented distribution of >10,000 km².
Undetermined	Taxa for which there is insufficient taxonomic framework available to provide any informed comment on the species-level distribution of the fauna or, therefore, the risk of small-scale spatial restrictions.

3.3 SRE Survey Approach and Effort

SRE fauna was surveyed using two approaches:

1. targeted searches undertaken during detailed and targeted terrestrial fauna surveys; and
2. systematic pitfall trapping during detailed vertebrate fauna surveys, when invertebrate specimens were captured as bycatch.

SRE sampling was undertaken in conjunction with two detailed vertebrate fauna surveys (using the above two methods) and one targeted SRE fauna survey (using targeted searches only); amounting to a total of seven survey phases conducted between August 2017 and May 2024 (Table 3.2).

The total SRE survey effort expended across the Winu and AREH projects combined is summarised in Table 3.2 and presented in Figure 3.1 and amounts to:

- 62 targeted SRE search sites, and
- 68 pitfall trapping sites.

The SRE survey effort undertaken specifically *within the Winu DE* amounts to a total of 38 pitfall trapping sites and 19 targeted SRE search sites (Table 3.2). Over 96 person hours were spent on SRE fauna searches across both projects combined, and 32 of these person hours were spent searching within the DE.

All surveys were completed by qualified and suitably experienced Biota zoologists, as detailed in (Biota 2018, 2021, 2022) and summarised below in Table 3.3. We acknowledge the support and guidance of all Traditional Owner rangers who participated in and assisted with surveys on country.

Table 3.2: Consolidated SRE survey effort for Winu and AREH projects in relation to Winu DE.

Survey	Area Surveyed	Survey Timing	Total Pitfall Trap Sites [no. within DE]	Total SRE Search Sites [no. within DE]	Total SRE Search Effort (person minutes) [effort within DE]
AREH Detailed (Biota 2018, 2022)	RAC and surrounds	1. Phase 1: 24/08 – 05/09/2017 2. Phase 2: 13 – 21/03/2018 3. Phase 3: 8 – 19/03/2021	48 [20]	29 [3]	1,364 [120]
Winu Detailed (Biota 2021)	MIA	1. Phase 1: 12 – 20/05/2019 2. Phase 2: 18 – 25/09/2019	20 [18]	17 [11]	3,039 [1,449]
Winu Borefields Targeted SRE	1. RAC and surrounds 2. Rimfire and surrounds	1. 26/02- 04/03/2024 2. 07-13/05/2024	0	16 [5]	1,404 [372]
Total [within DE]			68 [38]	62 [19]	5,807 [1,941]

Table 3.3: Summary of field survey personnel on SRE fauna surveys related to the Winu Project.

Team member	Role	Years of experience	AREH Detailed (Biota 2018, 2022)	Winu Detailed (Biota 2021)	Borefields Targeted SRE
Roy Teale	Field team leader	32	•	•	-
Michael Greenham	Field team leader	22	•	-	•
Dr Stewart Ford	Field team leader	20	•	•	-
Daniel Kamien	Field team leader	20	•	-	-
Peter Kendrick	Survey Zoologist	40	•	-	-
Dave Kierle	Survey Zoologist	15	•	-	-
Penny Brooshooft	Survey Zoologist	15	•	•	-
Dr Sylvie Schmidt	Survey Zoologist	12	•	-	-
John Graff	Survey Zoologist	12	•	•	-
Jacinta King	Survey Zoologist	10	•	•	-
Joshua Keen	Survey Zoologist	7	•	•	-
Nathan Beerkens	Survey Zoologist	7	•	•	-
Hayley Winter	Survey Zoologist	3	-	-	•

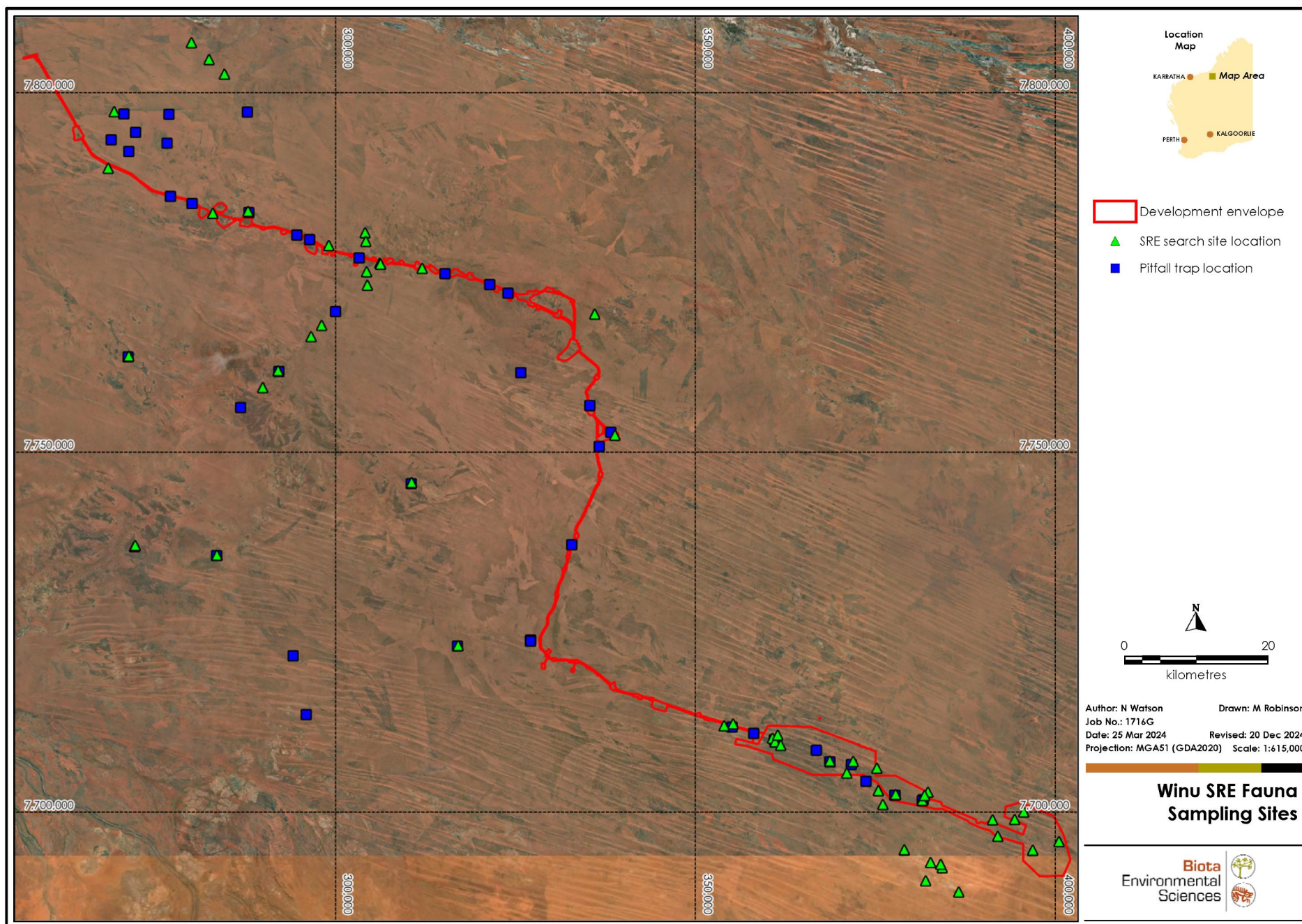


Figure 3.1 SRE search sites and pitfall trap locations in relation to the Winu DE.

3.4 Survey Conditions

3.4.1 Weather and Climate

Given the remote location of the Winu project, the closest weather station that can provide a robust dataset of long-term climatic conditions is the Bureau of Meteorology (BoM) weather station at Telfer Aero (No. 013030), located approximately 115 km southeast of the survey area. Figure 3.2 depicts the monthly average rainfall, maximum and minimum temperatures with their respective long-term median values (lighter coloured lines and columns) for the years surveys have taken place.

The weather conditions experienced during and preceding a survey period can influence survey findings, particularly for some invertebrate fauna groups that become more active in moist or humid conditions (i.e. land snails, millipedes and ‘wandering’ male mygalomorph spiders which are often collected in pitfall traps). Weather conditions at the time of each survey are detailed in the individual survey reports (Biota 2018, 2021, 2022) but in summary:

- Conditions during all three phases of the AREH detailed survey were typical of the region at the time of each survey, though significant rainfall events occurred in the months preceding Phase 1 (January and February 2017) and Phase 2 (January and February 2018).
- For the Winu detailed survey, Phase 1 occurred after an unusually dry wet season (January - March), with much lower rainfall recorded than the long-term medians across each month.
- The two targeted borefield phases in March and May 2024 were both preceded by higher than average rainfall. Some areas were also significantly burnt.

Across the years surveys have taken place, significant high rainfall events occurred in December and January 2017 (preceding the AREH Phase 2 survey), in March and May 2022, April 2023 and also January and March 2024 (preceding both phases of the targeted surveys of the borefields)(see Figure 3.2). Rainfall was much lower than the median across the wet season months in 2019. Generally, average minimum and maximum monthly temperatures hovered close to that of the long-term medians, but these average temperatures were notably exceeded in November 2018-February 2019, November 2019, December 2021 and February 2024. The year 2019 experienced drought conditions with higher maximums and minimum temperatures recorded, particularly across the early summer months.

3.4.2 Fire History

Fire has played a dominant role in shaping many of Australia’s ecosystems, particularly desert landscapes. The DE has been directly impacted by fire multiple times since biological survey work began. Fire occurrences in the DE are described briefly below (Table 3.4) and mapped in Figure 3.3 (data from Northern Australia & Rangelands Fire Information (NAFI)):

Table 3.4: Summary of the fire history of the Winu DE.

Area (ha)	Year burnt	Approximate area burnt (ha)
MIA	2018	6,663
	2022	1,797
	2023	3,035
RAC	2017	836
	2018	2,626
	2019	1,388
	2022	170
	2023	2,923
Rimfire	2018	6,678
	2023	173

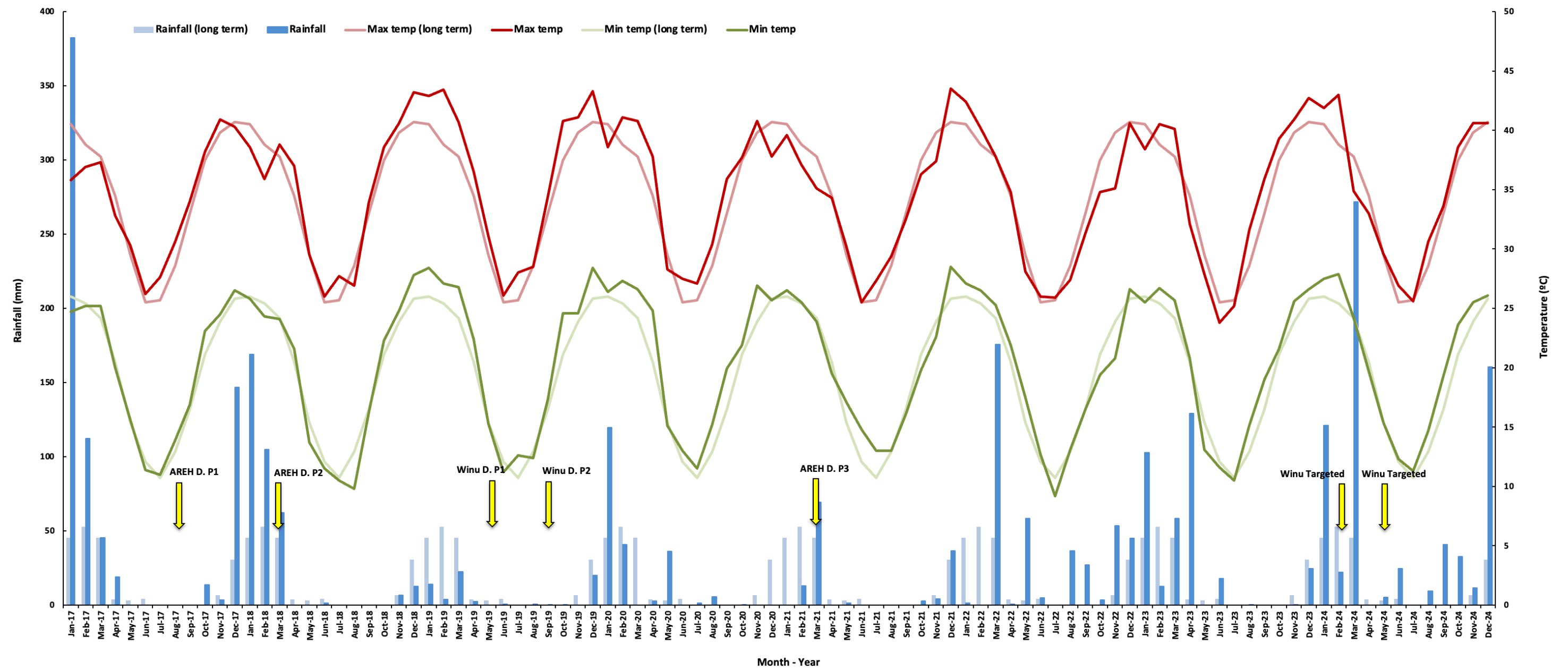


Figure 3.2: Climate graph depicting long-term averages and monthly data for the Telfer Aero (#013030) weather station (data from BoM) for the years surveys took place in the Winu DE.

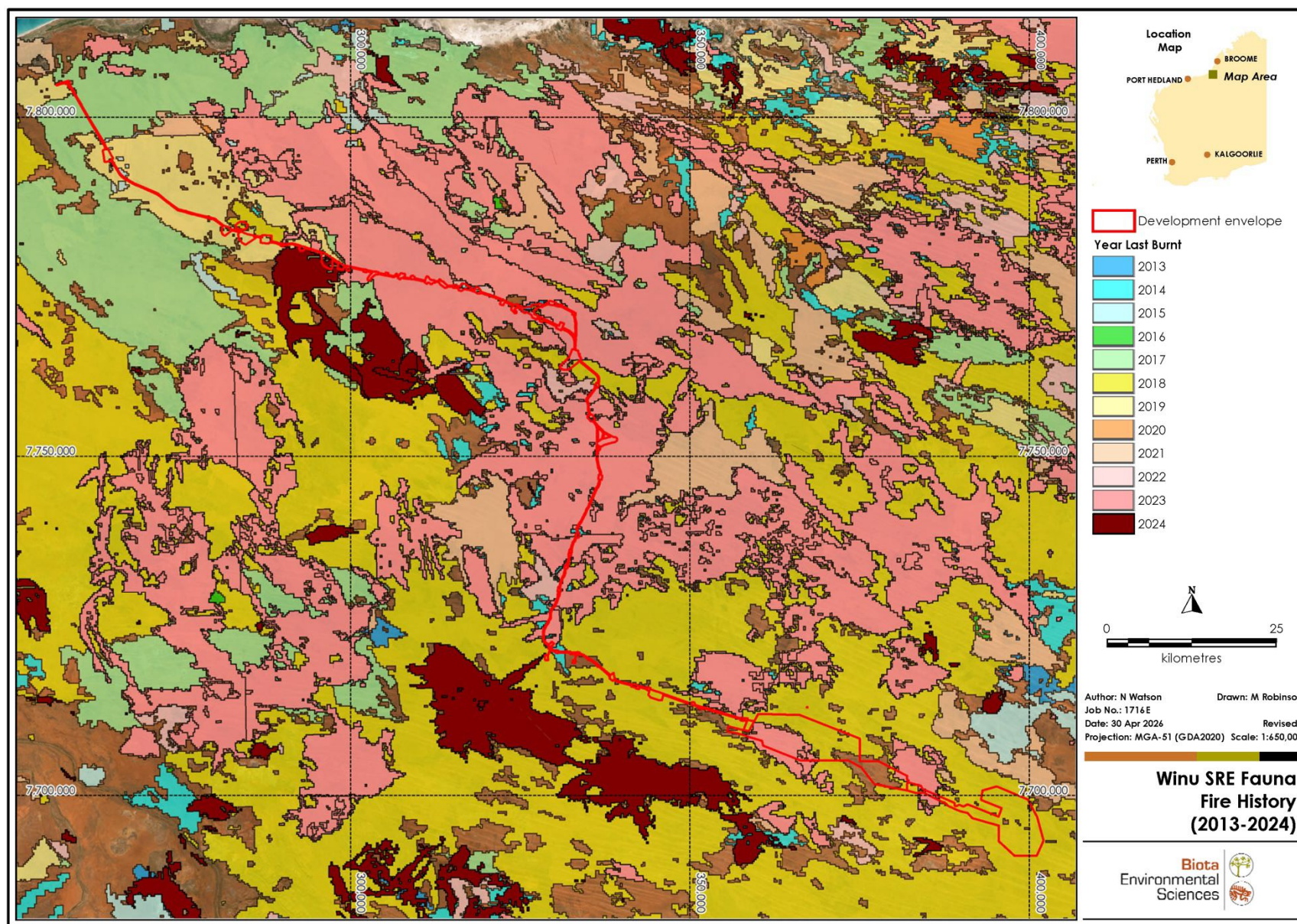


Figure 3.3: Fire scar history of the Winu DE and surrounding locality.

3.5 Target Taxa and Sampling Methodology

Based on the results of the desktop study, a review of habitats available and consultation with the WA Museum, the following groups were considered likely for the locality and therefore targeted during the surveys:

- Mygalomorphae (trapdoor spiders);
- Scorpionida (scorpions);
- Pseudoscorpionida (pseudoscorpions);
- Diplopoda (millipedes); and
- Pulmonata (land snails).

Search methodologies employed during the targeted searches and specimen processing procedures for each targeted group are detailed in Table 3.5.

Table 3.5 Target taxa, survey methodology and specimen processing procedures.

Target Taxa	Survey Methodology	Specimen Processing
Mygalomorph Spiders	Mygalomorph spider burrows were located by: • Visually searching prospective habitats, the surface layer of dirt and leaf litter was removed to reveal any camouflaged mygalomorph burrows; • A hole was dug adjacent to each burrow, allowing the burrow to be followed down with forceps until the spider was located; • Spiders were also opportunistically collected from pitfall traps.	Two legs of each individual collected removed and placed in 100% ethanol for molecular studies, while remainder of the specimen preserved in 70% ethanol for morphological studies. Juveniles split into two groups with some preserved in 100% ethanol for molecular studies and the remainder placed in 70% ethanol for morphological studies. Individuals found dead or accidentally damaged during collection were immediately preserved in 100% ethanol.
Scorpions	Scorpions were located by: • Visual searches in prospective habitat; • Scorpions were also collected opportunistically (e.g. while excavating mygalomorph spider burrows) and from pitfall traps.	
Pseudoscorpions	Searches for pseudoscorpions were conducted by: • searching on trees and beneath bark; • searching under rocks; and • raking and sieving soil and leaf litter.	
Millipedes	Millipedes were located by: • searching under rocks; and • raking/sieving soil and leaf litter.	Individuals preserved as whole specimens in 100% ethanol for molecular studies.
Snails	Searches for land snails were conducted by: • excavating leaf litter and soil around the base of spinifex (<i>Triodia</i>) hummocks; • searching under rocks and in rock crevices and pools; and • raking/sieving soil and leaf litter.	Land snails kept aestivating (in dry calico bags) until commencement of molecular analysis.

3.6 Genetic Analysis of Specimens

Molecular (DNA) analysis of invertebrate specimens was undertaken to determine the number of species present, place them into local and regional context where possible and better assess their SRE status. Molecular analyses were undertaken by Helix Molecular Solutions Pty Ltd (Helix), with methodology detailed in Appendix 1.

3.7 Survey Limitations

In accordance with the EPA (2016), potential constraints and limitations of the SRE surveys were addressed in each of the supporting reports. As this report collates data from multiple source studies, the limitations that apply to each of those also apply here. These comprise:

- Sampling effort and methods were not equal amongst the consolidated surveys, as survey timing spanned a variety of sampling seasons and differing habitats were represented. Each individual supporting study was, however, adequate to meet relevant policy expectations for the nature of the survey.
- Contextual information at a regional and local level is limited for SRE species in the Great Sandy Desert.
- Disturbance (fire) was a significant factor in some parts of some of the survey areas.
- This report concerns SRE invertebrate fauna only. Vertebrate fauna sampling was also conducted in the survey areas and is reported on in Biota (2025)
- Not all parts of the survey areas were ground-truthed or systematically sampled, as parts of some survey areas were inaccessible. Dune access was also restricted during some surveys due to heritage considerations.

4.0 Existing Environment

A summary of bioregional information relevant to the extent of the DE is presented here. For more detail in relation to the RAC and MIA, refer to the desktop studies in the source reports cited in Section 3.1.1.

4.1 Native Title

The DE encompasses two Native Title determination areas; the Nyangumarta Native Title determination in the north (overlapping 70 % of the MIA), and the Martu Native Title determination in the south. The RAC is entirely included in the Nyangumarta Native Title determination and Rimfire is entirely in the Martu Native Title determination.

4.2 IBRA Bioregion

The Interim Biogeographic Regionalisation of Australia (IBRA) identifies 89 bioregions across Australia (Environment Australia 2000). The RAC, MIA, and Rimfire are located within the Great Sandy Desert IBRA bioregion, which is characterised by red sand plains, dune fields and remnant rocky outcrops. Vegetation is predominantly spinifex grasslands, low woodlands and shrubs. The Great Sandy Desert IBRA bioregion is divided into six subregions, of which two are relevant to the Winu DE: the Mackay and McLarty subregions. The MIA and Rimfire are located entirely within the Mackay subregion, and the RAC extends from the Mackay subregion in the south, through the McLarty subregion, with a small portion of the northern extent within the Pindanland subregion of the Dampierland bioregion. These three subregions are summarised below.

- The Mackay subregion (18,636,695 ha) comprises the “tropical inland 'red-centre' desert, and includes the 'Percival' and 'Auld' palaeoriver systems”. Mainly tree steppe grading to shrub steppe in south; comprising open hummock grassland of *Triodia pungens* and *Triodia schinzii* with scattered trees of *Owenia reticulata* and bloodwood (*Corymbia* spp.), and shrubs of *Acacia* spp., *Grevillea wickhamii* and *G. refracta*, on Quaternary red longitudinal sand dune fields. The climate is arid tropical with summer rainfall, and monsoonal influences are apparent in the northwestern sector of this region” (Kendrick 2003). The vegetation is similar to the McLarty subregion.
- The McLarty subregion (13,173,266 ha) “includes the Mandora palaeoriver system and red-brown dunefields with finer texture than further south. It also includes gravelly surfaces of Anketell Ridge along its northern margin. The subregion is arid tropical with summer rain and is influenced by monsoonal activity. Morning fogs are recorded during the dry season. The vegetation is mainly tree steppe grading to shrub steppe in the south; comprising open hummock grassland of *Triodia pungens* and *Triodia schinzii* with scattered trees of *Owenia reticulata* and Bloodwoods (*Corymbia* spp.), and shrubs of *Acacia* spp., *Grevillea wickhamii* and *G. refracta*, on Quaternary red longitudinal sand dune fields overlying Jurassic and Cretaceous sandstones of the Canning and Amadeus Basins. Gently undulating lateritised uplands support shrub steppe” (Graham 2003a). Wetland features in the subregion include isolated mound springs supporting *Melaleuca leucadendra* closed forests, and *Melaleuca glomerata* - *M. lasiandra* shrublands around salt lakes (Graham 2003a).
- The Pindanland subregion (5,198,904 ha) “comprises sandplains of the Dampier Peninsula and western part of Dampier Land, including the hinterland of the Eighty Mile Beach. It is a fine-textured sand-sheet with subdued dunes and includes the paleodelta of the Fitzroy River. This is the coastal, semi-arid, northwestern margin of the Canning

Basin. The climate is described as dry hot tropical and semi-arid with summer rainfall. The average annual rainfall is between 450 – 700 mm, slightly lower than the Fitzroy Trough subregion” (Graham 2003b). The vegetation is described primarily as pindan, but includes *Melaleuca alsophila* low forests on coastal plains, and *Spinifex* spp. – *Crotalaria* spp. strand communities (Graham 2003b).

4.3 Surface Geology

Mapping of the surface geological units in the locality of Winu was prepared based on data from Geoscience Australia (2014). The majority of the DE (67%) is dominated by dune geology (Qd), with smaller areas of sandstone and siltstone with interbedded conglomerate (Ksak). The northern section of the RAC and MIA consist of a mosaic of the broadly dominant sand plains (Czs), intersected with numerous small sections of ferruginous duricrust laterite (Czl), and fluviatile sandstone conglomerate (JKsc). The southern section of the MIA and Rimfire consist of both sand plain (Czs), and sand dune (Qd) geology.

4.4 Land Systems and Soil Landscapes

The then Department of Agriculture Western Australia mapped land systems for the Rangelands regions of WA (DAFWA 1994), including much of the study area (with the boundary ending 11.2 km from the MIA’s western extent (van Vreeswyk et al. 2004)). This classification divides the region into broad units (land systems), each consisting of a series of “land units” that occur on characteristic physiographic types within the land system.

Four land systems have been mapped as occurring in the DE (Table 4.1; Figure 4.1). The southern portion of the RAC is dominated by the Little Sandy land system, while the northern section is a mosaic of the Nita and Callawa land systems, with the Buckshot land system being present in two small areas (Figure 4.1). The MIA is entirely represented by the Little Sandy system (Figure 4.1). For all land systems, and their subordinate land units, the extent within the DE represents <0.5% of their subregional occurrence and the land systems are very extensive and well-represented at regional scale.

The land system mapping does not extend east of the MIA, thereby excluding the Rimfire borefield. For these areas, soil-landscape mapping by DPIRD (2018) was instead utilised to characterise the landscape (Table 4.1; Figure 4.1).

Five broad soil landscapes have been mapped in the DE (DPIRD 2018). Unit AB39 and AB40 are represented around the MIA, with both units described as gently undulating plains with longitudinal dunes, however AB40 is more elevated in the landscape than AB39. Unit AB21 and AB22 are similarly described as gently undulating sand plains, however AB22 features many rocky sandstone residuals. These two units are represented around the RAC, in addition to unit AB39 (Figure 4.1). Rimfire is predominantly represented by unit AB40; gently undulating plains with longitudinal dunes with geological unit B30, dune fields with areas of clay pans and salt pans, overlaps the Rimfire corridor (Figure 4.1).

Table 4.1: Land system and soil landscape units within the DE.

Mapping system	Mapping unit	Description	Area (Ha)	Proportion of DE (%)
Land system	Little Sandy System	Sandplains with linear and reticulate dunes supporting shrubby hard and soft spinifex grasslands	11,838.44	50.06
Soil landscape	AB40	Gently undulating plains with longitudinal dunes	7,241.12	30.62
Soil landscape	B30	Dune fields with areas of clay pans and salt pans	191.77	0.81
Land system	Nita System	Sandplains supporting shrubby spinifex grasslands with occasional trees.	2,221.47	9.39
Land system	Callawa System	Highly dissected low hills, mesas and gravelly plains of sandstone and conglomerate supporting soft and hard spinifex grasslands	2,060.25	8.71
Land system	Buckshot System	Gravelly sandplains and occasional sand dunes supporting hard spinifex grasslands	95.98	0.41
Total			23,649.03	100

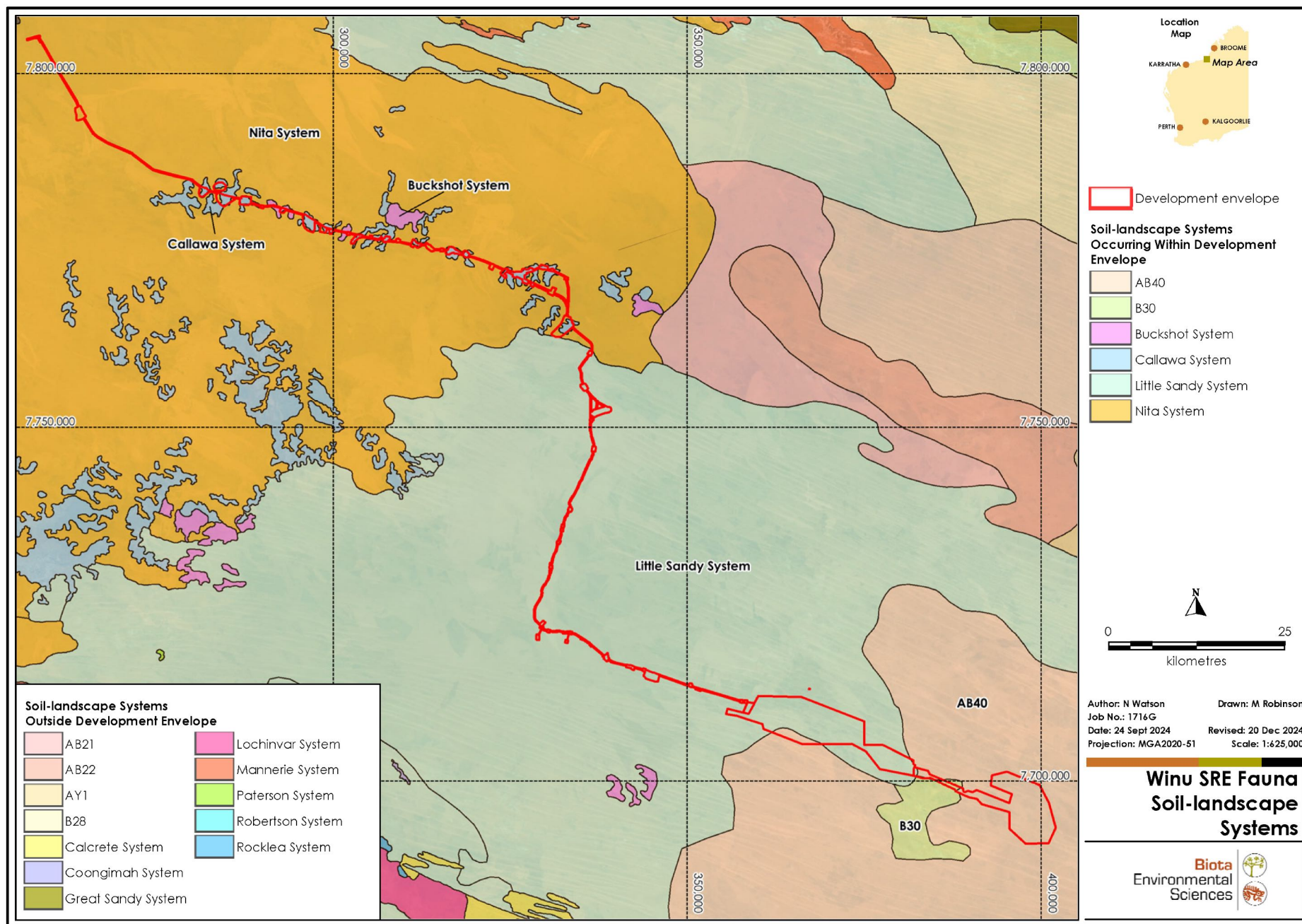


Figure 4.1: Land systems and soil landscapes of the Winu DE and surrounds.

4.5 Soils

Soil units in relation to the Winu DE were mapped using the Atlas of Australian Soils (Agriculture Western Australia 1967). Though there is some overlap between this mapping system and the DPIRD (2018) soil landscape mapping, the soil mapping provides additional detail and identifies finer-scale variation in soil types.

Five soil units occur within the DE (Table 4.2; Figure 4.2). Units AB39 and AB40 are the most abundant within the DE, representing undulating sandplains dominated by longitudinal dunes (Table 4.2; Figure 4.2). These units are present midway along the RAC, throughout the MIA and across the majority of Rimfire (Figure 4.2). Units AB21 and AB22, gently undulating sandplains with sandstone residuals, occur across the mid- and western portion of the RAC. Unit B30 represents less than 1% of the DE, overlapping the Rimfire pipeline corridor and extending south of the DE (Figure 4.2).

Table 4.2: Soil units within the DE.

Soil unit	Description	Area (Ha)	Proportion of DE (%)
AB39	Gently undulating plain dominated by longitudinal dunes of varying frequency; some exposures of ironstone gravels on low rises occur in the dune swales: chief soils are red earthy sands (Uc5.21) on dune slopes, and interdune plains with red siliceous sands (Uc1.23) on the dunes. Other soils include (KS-Uc5.21) on the gravelly rises where an ironstone (laterite) duricrust is present at about 18 in. depth; and (Um5.11) on small included areas of calcrete (kunkar).	10,841.01	45.84
AB40	Gently undulating plain slightly more elevated than unit AB39, and dominated by longitudinal dunes, many exposures of ironstone gravels and some breakaways capped by ironstone (laterite) duricrust: chief soils are red earthy sands (Uc5.21), with red siliceous sands (Uc1.23) on the dunes. There is an increased amount of (KS-Uc5.21) soil compared with unit AB39, and locally it may become dominant.	7,240.67	30.62
AB22	Gently undulating sand plain as for unit AB21 but with many rocky sandstone residuals: chief soils are red earthy sands (Uc5.21), with (Uc5.11) and (Uc1.23) as for unit AB21. Associated are bare rock and shallow sands, probably (Uc1.4), of the sandstone residuals.	3,625.24	15.33
AB21	Pindan country - gently undulating sand plain with a few small rocky sandstone residuals; no external drainage: chief soils are red earthy sands (Uc5.21), with associated (Uc5.11) and hummocks of siliceous sands (Uc1.23).	1,750.46	7.40
B30	Dune fields as for unit B28 but with considerable areas of clay pans and salt pans: chief soils are probably red siliceous sands (Uc1.23) together with (Uc5.21) sands as for unit B28, but locally with more extensive areas of (Dy1.33), (Dy1.43), probably similar (Dr1) soils, and (Uf) or (Ug) soils.	191.65	0.81
Total		23,649.03	100

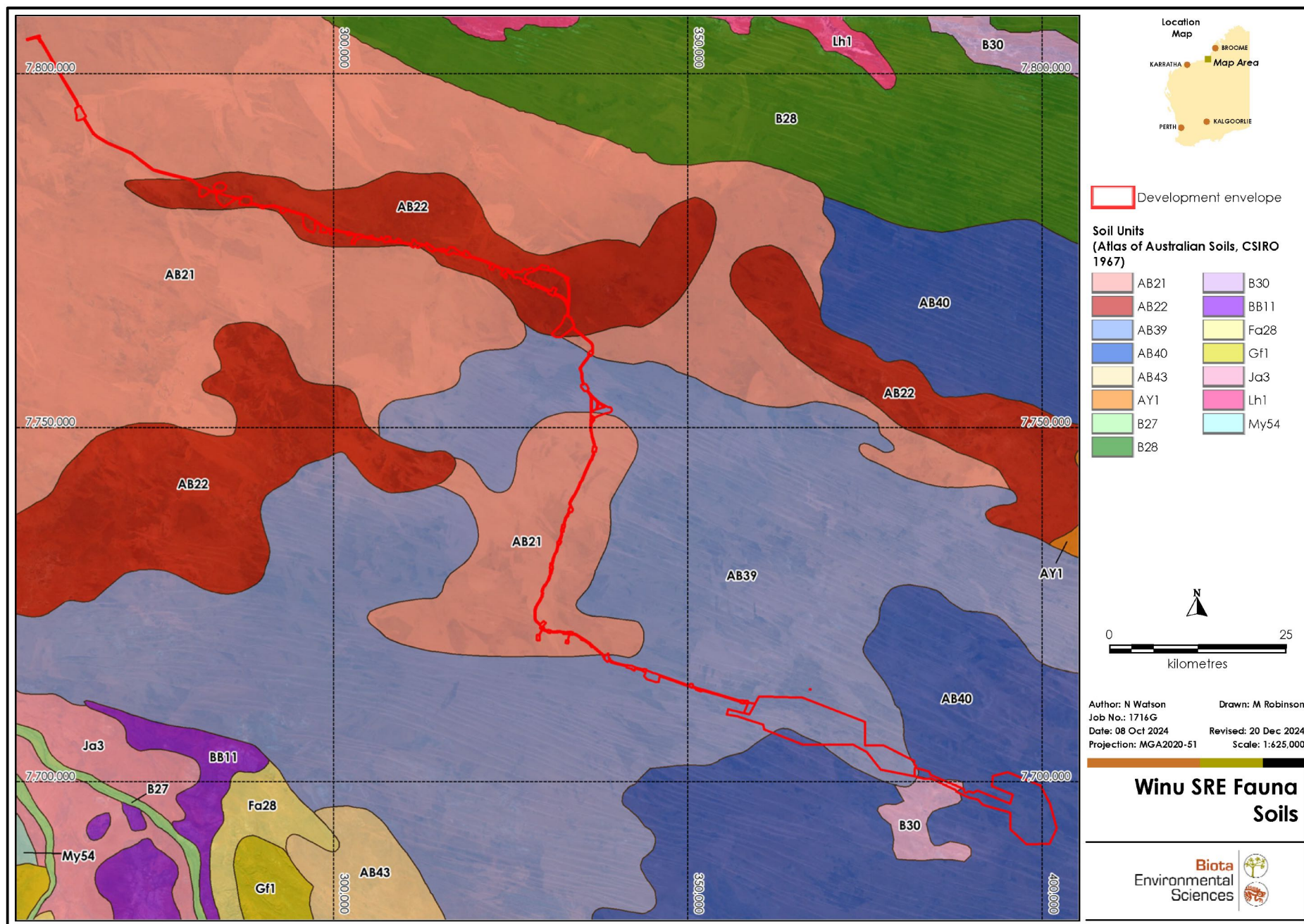


Figure 4.2: Soil units of the Winu DE and surrounds.

4.6 Dune Landforms

An assessment of the significance of the dunal landform within the MIA was undertaken by SLR Consulting Australia (SLR Consulting 2024). Morphological analyses of shape, slope and aspect revealed no significant difference between the dunal landform within the MIA to four comparison sites, and more broadly to those in the Little Sandy Desert System. The dunal landform within the MIA is well represented at a local and regional scale, and is not considered to meet the EPA's criterion for scientific importance (EPA 2015).

The similarities between the landforms in the MIA and those in the surrounding area indicate that any microhabitats that are present in the dune landforms of the MIA are likely to also be present in the dune landforms throughout the region (SLR Consulting 2024).

4.7 Previous Records of Invertebrate Fauna

The database searches detailed in Section 3.1.1 returned no invertebrate records of conservation significance within a 100 km radius of the DE. The invertebrate records returned within the search area were then reviewed for their likelihood to represent SRE fauna using the criteria outlined in Section 3.2, and their assessed SRE status is presented in Table 4.3.

The majority of the database records comprised collections from AREH and Winu (Biota 2018, 2021, 2022)(discussed in this report), in addition to collections of spiders and scorpions from the Pilbara Biological Surveys (PBS) (Durrant et al. 2010, Volschenk et al. 2010). Many of the records from the PBS still remain undescribed, only being identified to either family or genus level. Of those that have been formally described, only two represent potential SRE fauna based on currently available information; the mygalomorph spider species *Aname muniyardae* and *Aname nitidimarina*, both of which have only been collected from, or near, Warrawagine Homestead near the western edge of the Great Sandy Desert IBRA bioregion (approximately 85 km west of the MIA) (Castalanelli et al. 2020). The remaining mygalomorph spider taxa previously recorded within the desktop search area were only identified to family or genus level; *Barychelidae* sp., *Conothele* sp. and *Missulena* sp.. These taxa can be conservatively assessed as also representing potential SRE fauna due to short-range endemism being common in their family/genera, however no further discussion beyond that is currently possible without further analysis. The locations of the five taxa identified during the desktop study as potential SRE fauna are shown in Figure 4.3.

Table 4.3: SRE assessment of invertebrates previously recorded within desktop search area.

CLASS Order Family	Taxa	SRE Status
ARACHNIDA Araneae		
Anamidae	<i>Aname baileyorum</i>	Not SRE - Throughout eastern Pilbara (Castalanelli et al. 2020)
	<i>Aname ellenae</i>	Not SRE - Has been found along the northern coast of the Pilbara, but also along the Fortescue Marsh in the Central Pilbara (Harvey et al. 2012)
	<i>Aname muniyardae</i>	Potential SRE – Has only been collected from Warrawagine Homestead near the western edge of the Great Sandy Desert IBRA bioregion (Castalanelli et al. 2020)

CLASS Order Family	Taxa	SRE Status
	<i>Aname nitidimarina</i>	Potential SRE – Has only been collected from near Warrawagine Homestead near the western edge of the Great Sandy Desert IBRA bioregion (Castalanelli et al. 2020)
	<i>Aname sinuata</i>	Not SRE - Widely distributed throughout the Pilbara IBRA bioregion and adjacent Carnarvon, Great Sandy Desert and Little Sandy Desert (Castalanelli et al. 2020)
Barychelidae	Barychelidae sp.	Potential SRE (conservative assessment)
Halonoproctidae	<i>Conothele</i> sp.	Potential SRE (conservative assessment)
Actinopodidae	<i>Missulena rutraspina</i>	Not SRE
	<i>Missulena</i> sp.	Potential SRE (conservative assessment)
Selenopidae	<i>Karaops nyangumarta</i>	Not SRE (Crews 2013)
Scorpiones		
Buthidae	<i>Hemilychas alexandrinus</i> (<i>Lychas undulatus</i>)	Not SRE
Urodacidae	<i>Urodacus megamastigus</i>	Not SRE - widespread Pilbara and Shark Bay
	<i>Urodacus varians</i>	Not SRE - widespread Pilbara but likely a species complex

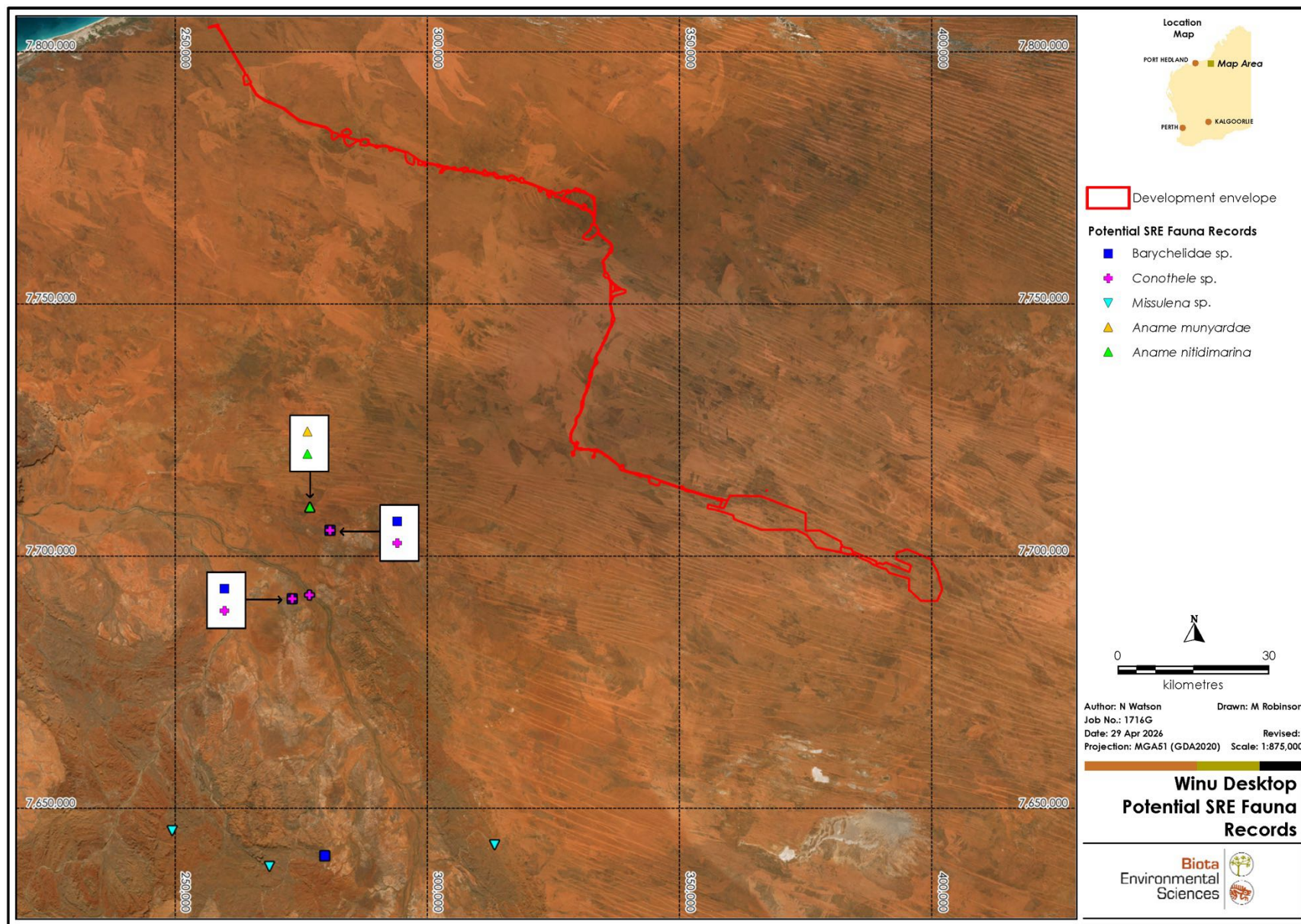


Figure 4.3: Desktop records of potential SRE fauna.

5.0 Results

5.1 Fauna Habitats

Five broad fauna habitats (plus disturbed/cleared areas) were identified based on the approach outlined in Section 3.1.2, in combination with on-ground habitat assessment and consideration of the ecological niches relevant to SRE fauna (Table 5.1; Figure 5.1). Just under three-quarters of the DE is represented by Shrub and spinifex on sandplain (~72%); Inland sand dune habitat represents 13% of the DE, as does Gravelly lateritic rises (also 13%). Ephemeral claypan habitat and Clayey sandplains with termitaria both represent less than 1% of the DE. Disturbed and cleared areas also make up less than 1% (Table 5.1; Figure 5.1). Descriptions of habitats and their possible values to SRE fauna are discussed in Table 5.2.

Table 5.1: Fauna habitat types and proportional representation of Winu DE.

Fauna Habitat	Area (ha)	Proportion (%)
Shrub and spinifex on sandplain	16,934.49	71.95
Inland sand dune	3,098.61	13.17
Gravelly lateritic rises	3,116.11	13.17
Ephemeral claypan	49.33	0.21
Disturbed/cleared area	212.21	0.90
Clayey sandplain with termitaria	124.74	0.53
Total	23,535.48	100

Table 5.2: Fauna habitats and their attributes within the Winu DE.

Habitat Description	Example Photograph
1. Shrub and spinifex on sandplain (72%)	
Description: Substrate consisted of pink to red pindan soils. The vegetation was dominated by <i>Corymbia zygomphylla</i>, <i>Erythrophleum chlorostachys</i> and <i>Owenia reticulata</i> trees over open to moderately dense mixed shrublands, typically dominated by wattles (<i>Acacia</i> spp.), over hummock grasslands of <i>Triodia schinzii</i> and <i>T. epactia</i>. Condition: Pre-2024 vegetation condition was excellent; fire impacted much of this fauna habitat type. SRE microhabitats: Limited: deposits of leaf litter and mature <i>Triodia</i> spp. hummocks provide some refuge for mesic and soil-dwelling groups.	
2. Inland sand dune (13%)	
Description: The sand dunes in inland areas had a pink to red pindan sand substrate and were typically long linear dunes trending east-west. These were dominated by mixed open shrublands over open hummock grasslands of <i>Triodia schinzii</i>. Condition: Excellent SRE microhabitats: Limited: deposits of leaf litter and mature <i>Triodia</i> spp. hummocks provide some refuge for mesic and soil-dwelling groups.	

Habitat Description	Example Photograph
3. Gravelly lateritic rises (13%)	
Description: Low rises with a surface covering of laterite gravel and pebbles occurred sporadically. These supported open hummock grasslands of <i>Triodia epactia</i> with a low open shrubland of the wattles <i>Acacia hilliana</i> and <i>A. adoxa</i> var. <i>adoxo</i>; taller shrubs were typically sparse but included species such as <i>Grevillea refracta</i> and <i>G. wickhamii</i>. Condition: Excellent SRE microhabitats: Limited: mature <i>Triodia</i> spp. hummocks provide some refuge for mesic and soil-dwelling groups.	
4. Clayey sandplain with termitaria (<1%)	
Description: Substrate comprised clayey sand to loose depth of 2 cm. The vegetation comprised <i>Acacia bivenosa</i> shrubland over <i>Triodia brizoides</i> open hummock grassland. Condition: Almost all had been recently burnt. SRE microhabitats: Extensive areas of higher clay-content soils are preferred habitat for some mygalomorph spider species (e.g. clay-lid trapdoor spiders).	
5. Ephemeral claypan (<1%)	
Description: Sandy clay loam plain in between dunes. Mixed spinifex groves. Condition: Excellent SRE microhabitats: Extensive areas of higher clay-content soils are preferred habitat for some mygalomorph spider species (e.g. clay-lid trapdoor spiders).	
6. Cleared/ Disturbed areas (<1%)	
Description: Road reserve Condition: Disturbed SRE microhabitats: None.	N/A

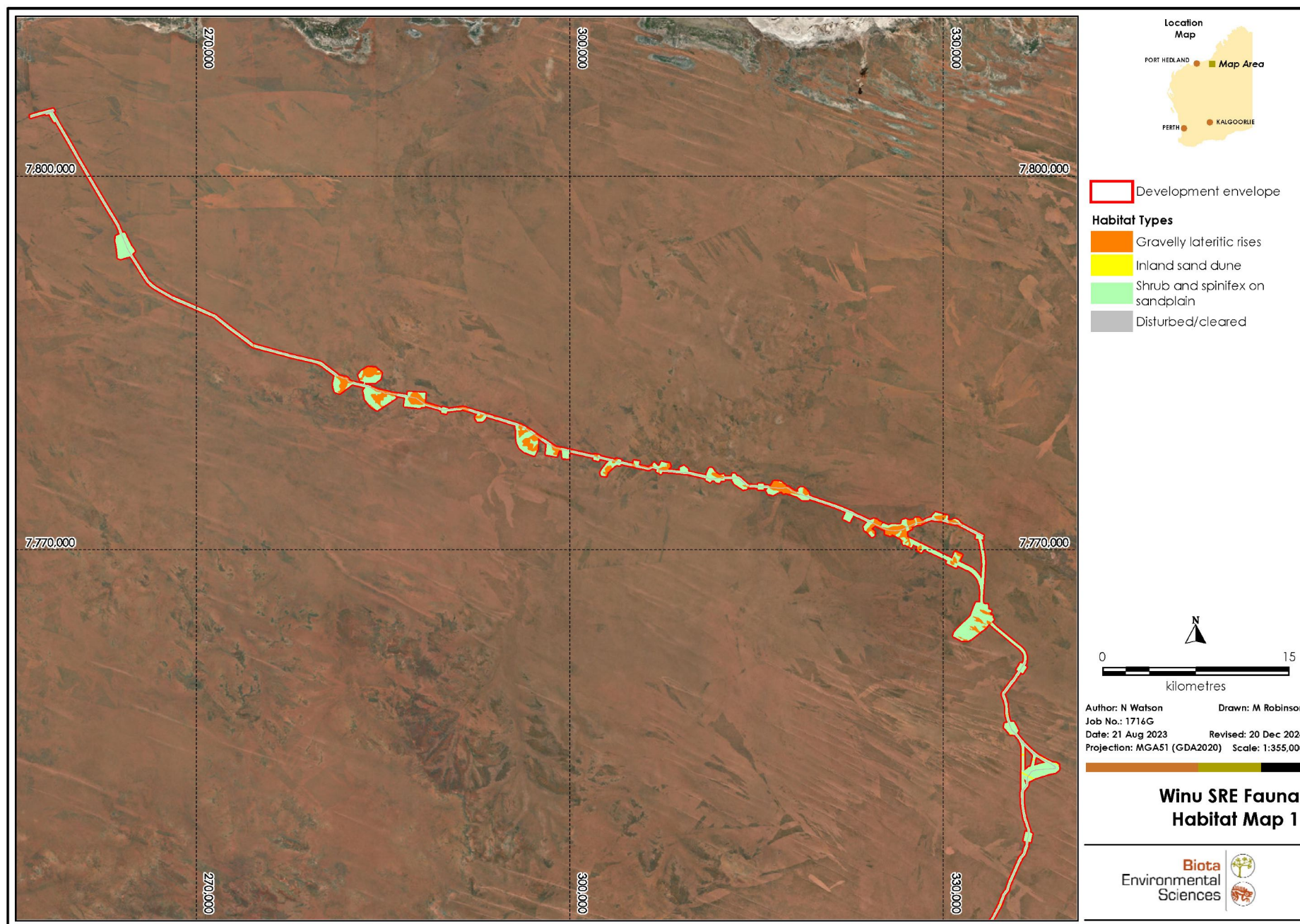


Figure 5.1: Fauna habitat mapping within the Winu DE (RAC section only).

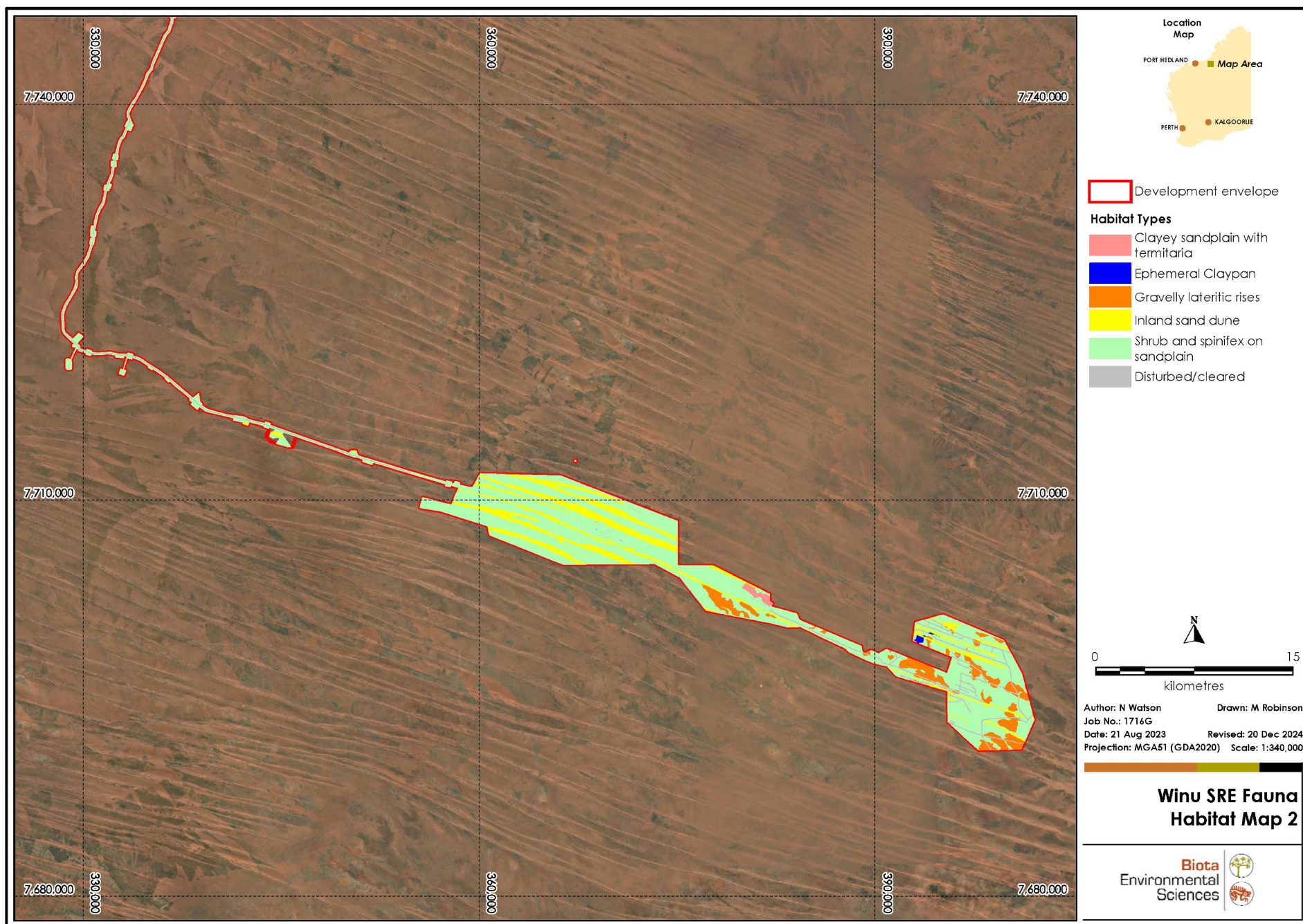


Figure 5.2: Fauna habitat mapping within the Winu DE (RAC, MIA and Rimfire).

5.2 Invertebrate Fauna Overview

The consolidated surveys recorded a total of 57 mygalomorph (trapdoor) spider and 23 scorpion specimens (Table 5.3; Appendix 2). These specimens have undergone molecular analysis and have been assigned a species-level identification (Section 5.2.1 - 5.2.2; Appendix 1).

Table 5.3 Summary of specimens collected within the Winu DE.

Survey	Spiders	Scorpions	Total
AREH Detailed	20	9	29
Winu Detailed	27	13	40
Borefields Targeted	10	1	11
Total	57	23	80

5.2.1 Mygalomorph Spiders

Of the 57 mygalomorph spiders submitted for molecular analysis, seven specimens failed to yield a viable DNA sequence and therefore could not be assigned to a genetic lineage. Four families were represented amongst the 50 sequenced specimens; Anamidae, Barychelidae, Halonoproctidae and Idiopidae (Section 5.2.1.1 - 5.2.1.4). A summary of the mygalomorph spider records is presented in Table 5.4, with the locations mapped in Figure 5.3.

5.2.1.1 Anamidae

Fourteen putative taxa belonging to the family Anamidae (previously Nemesiidae) were recorded, all of which are undescribed species (Table 5.4). Eleven of the 14 taxa belong to the genus *Aname*, the most speciose genus of the Anamidae family (Helix 2024). The remaining three anamid taxa not assigned to the genus *Aname* comprise one specimen identified as a new species within an undetermined genus (Genus? sp. N150), and two species of *Kwonkan* (spp. N151 and N197) (Table 5.4). Example burrow and specimen photos of the anamid species recorded are presented in Plate 5.1 - Plate 5.10.

Twelve of the 14 anamid taxa are newly recorded species and the following two species have been previously recorded outside of Winu;

- *Aname* sp. N7: the Winu specimens showed an affinity with this previously recorded species collected approximately 245 km southwest of Winu; and
- *Kwonkan* sp. H-N197: the Winu specimens represented a new lineage of this previously recorded species collected approximately 245 km west of the survey area (Helix 2024).

Due to the distances between the Winu specimens and the previous records of the same species, *Aname* sp. N7 and *Kwonkan* sp. H-N197 are not regarded as SRE taxa (Table 5.4). The remaining 12 anamid taxa are currently regarded as potential SRE taxa (Table 5.4; Section 6.0).



Plate 5.1 *Kwonkan* sp. N151 burrow
(M20190921.WINSRE12-01).



Plate 5.2 *Kwonkan* sp. N151
(M20190921.WINSRE12-01).



Plate 5.3 *Aname* sp. N147 burrow
(M20190518.WINSRE07-03).



Plate 5.4 *Aname* sp. N147
(M20190518.WINSRE07-03).



Plate 5.5: *Aname* sp. N153
(M20190923.WIN02P-01, pitfall
record).



Plate 5.6: *Aname* sp. N148
(M20190924.WIN01P-01, pitfall
record).



Plate 5.7: *Aname* sp. H-N206 burrow
(M20240301.WIB03SRE_MG_04).



Plate 5.8: *Aname* sp. H-N206
(M20240301.WIB03SRE_MG_04).

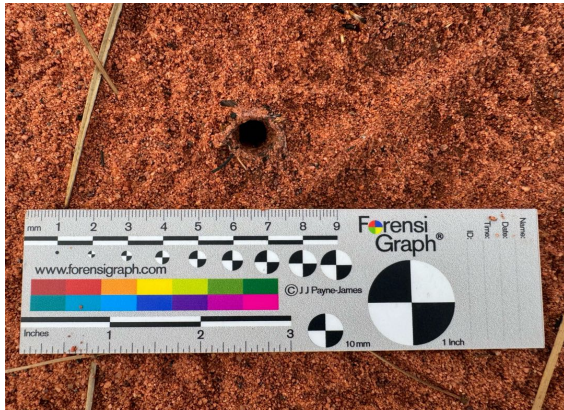


Plate 5.9: *Aname* sp. H-N206 burrow
(M20240301.WIB03SRE_MG-02).

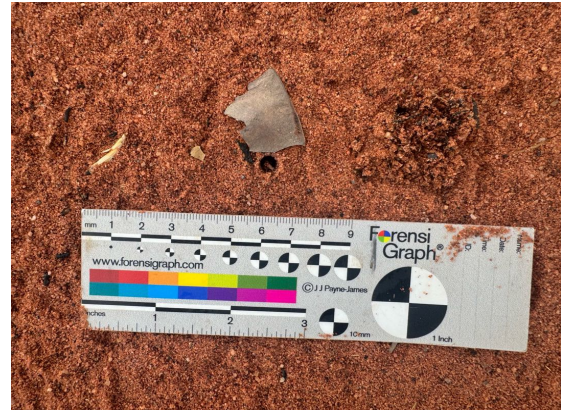


Plate 5.10: *Aname* sp. H-N206
(M20240301.WIB03SRE_MG-05).

5.2.1.2 Barychelidae

Two barychelid specimens were recorded, one from the eastern end of the MIA as pitfall bycatch, so burrow morphology is not known. Molecular analysis assigned this specimen to a previously unrecorded species within the genus *Idiommata* (*Idiommata* sp. B39) (Table 5.4). This species is currently regarded as a potential SRE.

The remaining barychelid specimen was recorded outside of the DE, south of the Rimfire pipeline corridor, from a burrow with a clay lid (Plate 5.11-Plate 5.12). This specimen did not sequence successfully and could not be assigned to a species. The SRE status of this species remains undetermined.

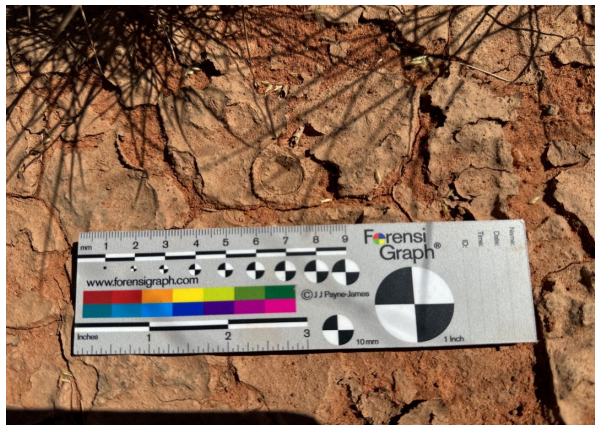


Plate 5.11: Barychelid sp. indet. burrow closed
(M20240513WIB11SRE_MG-02).

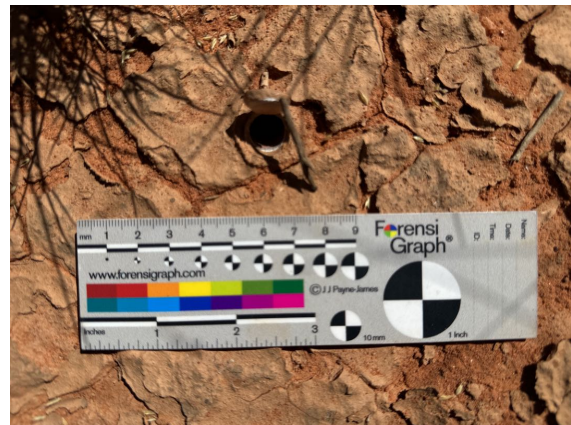


Plate 5.12: Barychelid sp. indet. burrow open
(M20240513WIB11SRE_MG-02).

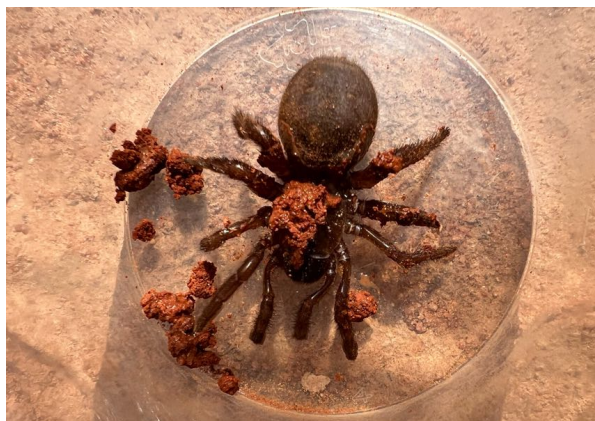


Plate 5.13: Barychelid sp. indet.
(M20240513WIB11SRE_MG-02).

5.2.1.3 Halonoproctidae

One specimen belonging to the family Halonoproctidae was recorded outside of the DE, south of the Rimfire pipeline corridor from a burrow with a clay lid (Plate 5.14 - Plate 5.16).

Molecular analysis assigned the specimen to a new lineage of a previously detected species, *Conothele* sp. H-C29, which is known from five specimens recorded from a location 290 km west (Helix 2024). This species is not considered likely to represent a SRE species.

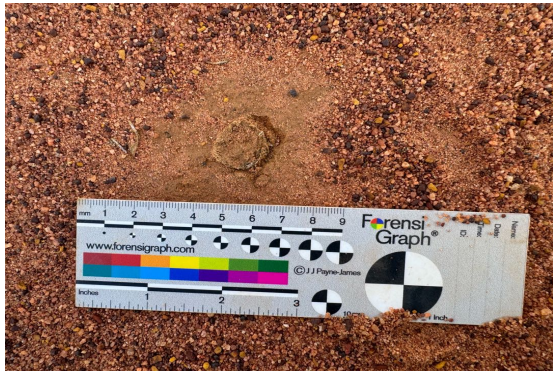


Plate 5.14: *Conothele* sp. H-C29 burrow closed (M20240513.WIB12SRE_MG-02).

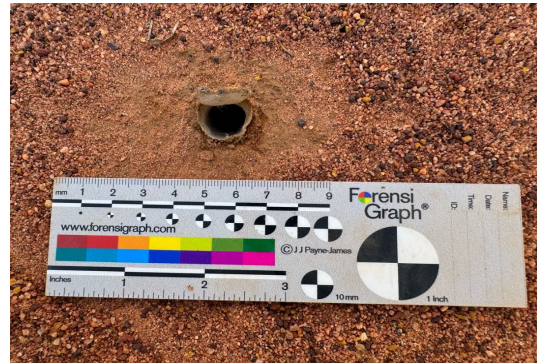


Plate 5.15: *Conothele* sp. H-C29 burrow open (M20240513.WIB12SRE_MG-02).



Plate 5.16: *Conothele* sp. H-C29 (M20240513.WIB12SRE_MG-02).

5.2.1.4 Idiopidae

Two idiopid specimens were recorded from outside of the DE, south of the Rimfire pipeline corridor, both from burrows with clay lids. Each specimen was assigned to a new species; *Idiosoma* sp. H-I90 and *Idiosoma* sp. H-I91 (Plate 5.17 - Plate 5.21) (Helix 2024). Both species are currently considered to represent potential SRE taxa.

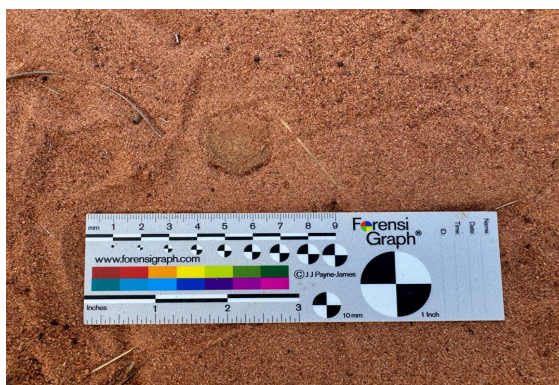


Plate 5.17: *Idiosoma* sp. H-I90 burrow closed (M20240513.WIB12SRE_MG-01).

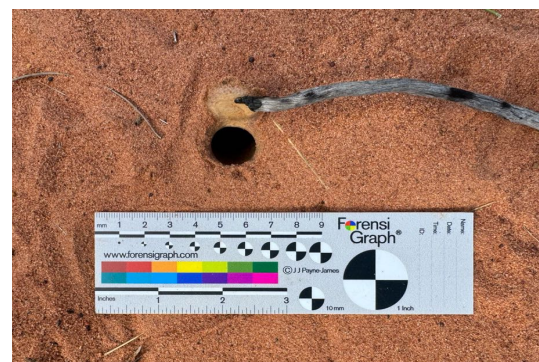


Plate 5.18: *Idiosoma* sp. H-I90 burrow open (M20240513.WIB12SRE_MG-01).



Plate 5.19: *Idiosoma* sp. H-I90
(M20240513.WIB12SRE_MG-01).

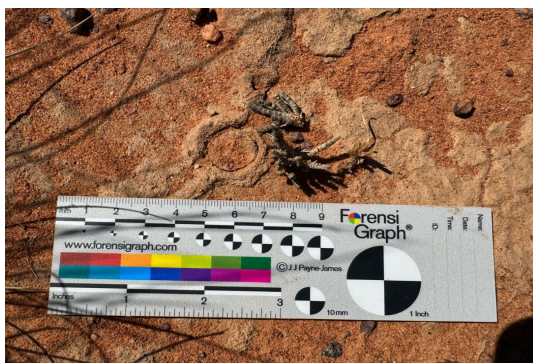


Plate 5.20: *Idiosoma* sp. H-I91 burrow closed
(M20240513.WIB11SRE_MG-01).

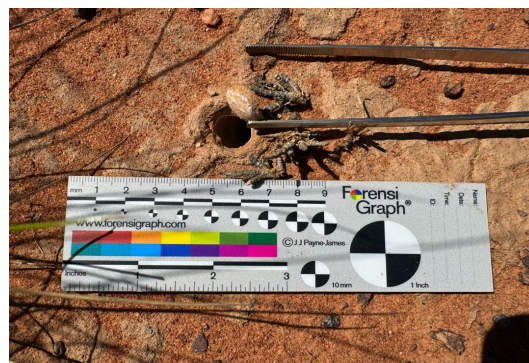


Plate 5.21: *Idiosoma* sp. H-I91 burrow closed
(M20240513.WIB11SRE_MG-01).

Table 5.4 Summary of mygalomorph spider records from Winu (taxa recorded solely within DE highlighted green).

Family	Molecular ID	Number of Specimens (Sites)	Region of DE	Fauna habitat	Distance between records	SRE status	Recorded outside DE?
Anamidae	<i>Aname</i> sp. N7	10(6)	RAC	Shrub and spinifex on sandplain	245 km between Winu & external records	Unlikely to be SRE	✓
	<i>Aname</i> sp. N138	2(1)	RAC	Shrub and spinifex on sandplain	Single site record	Potential SRE	✗
	<i>Aname</i> sp. N139	2(1)	RAC	Shrub and spinifex on sandplain	Single site record	Potential SRE	✓
	<i>Aname</i> sp. N140	1(1)	RAC	Shrub and spinifex on sandplain	Single site record	Potential SRE	✗
	<i>Aname</i> sp. N147	1(1)	MIA	Inland sand dune	Single site record 220 m outside DE	Potential SRE	✓
	<i>Aname</i> sp. N148	2(2)	MIA	Shrub and spinifex on sandplain, Inland sand dune	Two sites inside & outside DE, 338 m apart	Potential SRE	✓
	<i>Aname</i> sp. N149	1(1)	MIA	Inland sand dune	Single site record	Potential SRE	✗
	<i>Aname</i> sp. N152	3(1)	MIA	Shrub and spinifex on sandplain	Single site records	Potential SRE	✗
	<i>Aname</i> sp. N153	1(1)	MIA	Shrub and spinifex on sandplain	Single site record	Potential SRE	✗
	<i>Aname</i> sp. H-N205	1(1)	RAC	Shrub and spinifex on sandplain	Single site record	Potential SRE	✓
	<i>Aname</i> sp. H-N206	3(1)	RAC	Shrub and spinifex on sandplain	Single site records 300 m apart	Potential SRE	✓
	Genus? sp. N150	1(1)	MIA	Shrub and spinifex on sandplain	Single site record	Potential SRE	✗
	<i>Kwonkan</i> sp. N151	16(7)	MIA	Inland sand dune Shrub and spinifex on sandplain	Records inside & outside DE spanning 29.4 km	Potential SRE	✓
	<i>Kwonkan</i> sp. H-N197	2(1)	RAC	Shrub and spinifex on sandplain	245 km between Winu & external records	Unlikely to be SRE	✓
Barychelidae	<i>Idiommata</i> sp. B39	1(1)	MIA	Shrub and spinifex on sandplain	Single site record	Potential SRE	✗
	Barychelidae sp. – failed to sequence	1(1)	Outside	Shrub and spinifex on sandplain	N/A	Undetermined	✓
Halonoproctidae	<i>Conothele</i> sp. H-C29	1(1)	Outside	Shrub and spinifex on sandplain	290 km between Winu & external records	Unlikely to be SRE	✓
Idiopidae	<i>Idiosoma</i> sp. H-I90	1(1)	Outside	Shrub and spinifex on sandplain	Single site record	Potential SRE	✓
	<i>Idiosoma</i> sp. H-I91	1(1)	Outside	Shrub and spinifex on sandplain	Single site record	Potential SRE	✓
Unknown	Mygalomorphae sp. - failed to sequence	5(3)	RAC, MIA	Shrub and spinifex on sandplain	N/A	Undetermined	Not known
Total		57					

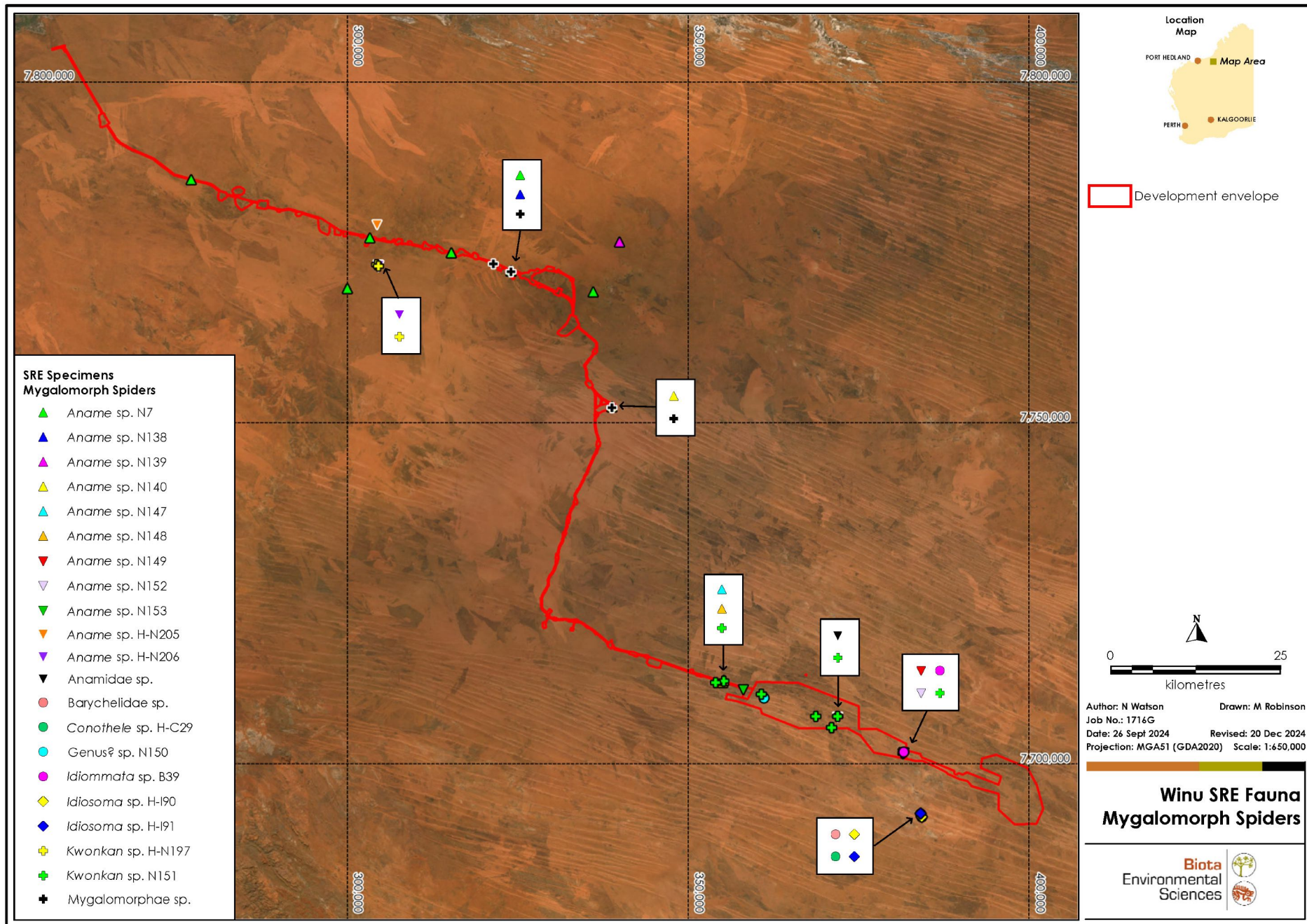


Figure 5.3: Location of spider fauna recorded in relation to the Winu DE.

5.2.2 Scorpions

Across all surveys within the DE, 23 scorpions were collected from two scorpion families, Buthidae and Urodacidae (see Section 5.2.2.1-5.2.2.2). Table 5.5 provides a summary of the scorpion records from Winu, with locations presented in Figure 5.4.

5.2.2.1 Buthidae

Eighteen specimens belonging to the family Buthidae were successfully sequenced, while one specimen failed to sequence and could not be assigned to a species.

Seventeen of the successfully sequenced specimens were placed within the species *Lychas annulatus* (also recognised as *Hemilychas alexandrinus*), which has a distribution extending across the arid zone of Australia and is therefore not an SRE. It is worth noting that scorpion taxonomy in Western Australia is not yet well-resolved and *Lychas annulatus* likely represents a species complex of several undescribed species. The species from Winu were assigned to two clades within the *Lychas annulatus* complex, which possibly represent separate taxa. However, without fuller taxonomic resolution, they are treated here as the formally described species *Lychas annulatus* (Plate 5.22).

The remaining successfully sequenced buthid specimen belonged to a separate clade of *Lychas* scorpions. The specimen showed 9.4% sequence divergence from the *L. annulatus* specimens, one of which was collected at the same locality. This level of divergence strongly indicates a separate species of *Lychas*. For resolution of this specimen, Dr. Erich Volschenk (of Alacran Environmental Science) was consulted to conduct further molecular analyses. Results from this analysis placed the specimen within the species *Lychas adonis*, which has a widespread distribution across arid parts of Australia and is therefore not an SRE (Plate 5.23).



Plate 5.22: *Lychas annulatus*
(S20190919.WIN01P-01).



Plate 5.23: *Lychas adonis*
(S20190919.WIN05P-01).

5.2.2.2 Urodacidae

Four of the five Urodacidae specimens were successfully sequenced, with three species detected; *Urodacus varians*, *Urodacus* sp. 'Telfer' and *Urodacus* 'yaschenkoi' species complex'.

The species *Urodacus varians* is a rarely collected dune specialist also known from the Gibson Desert. The distribution of this species is patchy, although it is thought to be present over much of central Western Australia. The species as currently described is not considered to be an SRE, although it may represent a species complex.

Two specimens were assigned to the undescribed species *Urodacus* sp. 'Telfer'. The specimens represented the fourth and fifth record of the species and the first female

specimens collected to date. However, only one was confirmed by sequencing, with the second identified based on morphology alone. The species was previously only known from an area south of Telfer and is therefore considered a potential SRE.

The remaining two urodacid specimens showed affinity to the species *Urodacus* 'yaschenkoi species complex', which is a species complex containing at least three putative species. The species complex is usually associated with red dune systems and has a collective distribution of central Queensland to WA Goldfields and Broome. The specimens from the MIA did not show affinity to any reference specimens within this species complex, and as such were considered a potential SRE species within the species complex.

Table 5.5 **Summary of scorpion records from Winu.**

Family	Molecular ID	No. Specimens (Sites)	Region of DE	Fauna habitat	Distance between records	SRE status	Recorded outside DE?
Buthidae	<i>Lychas annulatus</i> complex	16 (11)	RAC, MIA,	Inland sand dune, Shrub and spinifex on sandplain, Gravelly lateritic rises	68 km within Winu	Not SRE	✓
	<i>Lychas adonis</i>	1(1)	MIA	Inland sand dune	Single record	Not SRE	✓
	<i>Lychas</i> sp. - failed to sequence	1 (1)	MIA	Shrub and spinifex on sandplain	N/A	Undetermined	Not known
Urodacidae	<i>Urodacus varians</i>	1(1)	MIA	Shrub and spinifex on sandplain	Single record	Not SRE	✓
	<i>Urodacus</i> sp. 'Telfer'	2(1)	Rimfire	Inland sand dune	Single site record	Potential SRE	✓
	<i>Urodacus</i> 'yaschenkoi species complex'	2(1)	Rimfire	Inland sand dune	Single site record	Potential SRE	✓*
Total		23					

* Species complex recorded elsewhere but Winu specimens do not closely align with any in the complex.

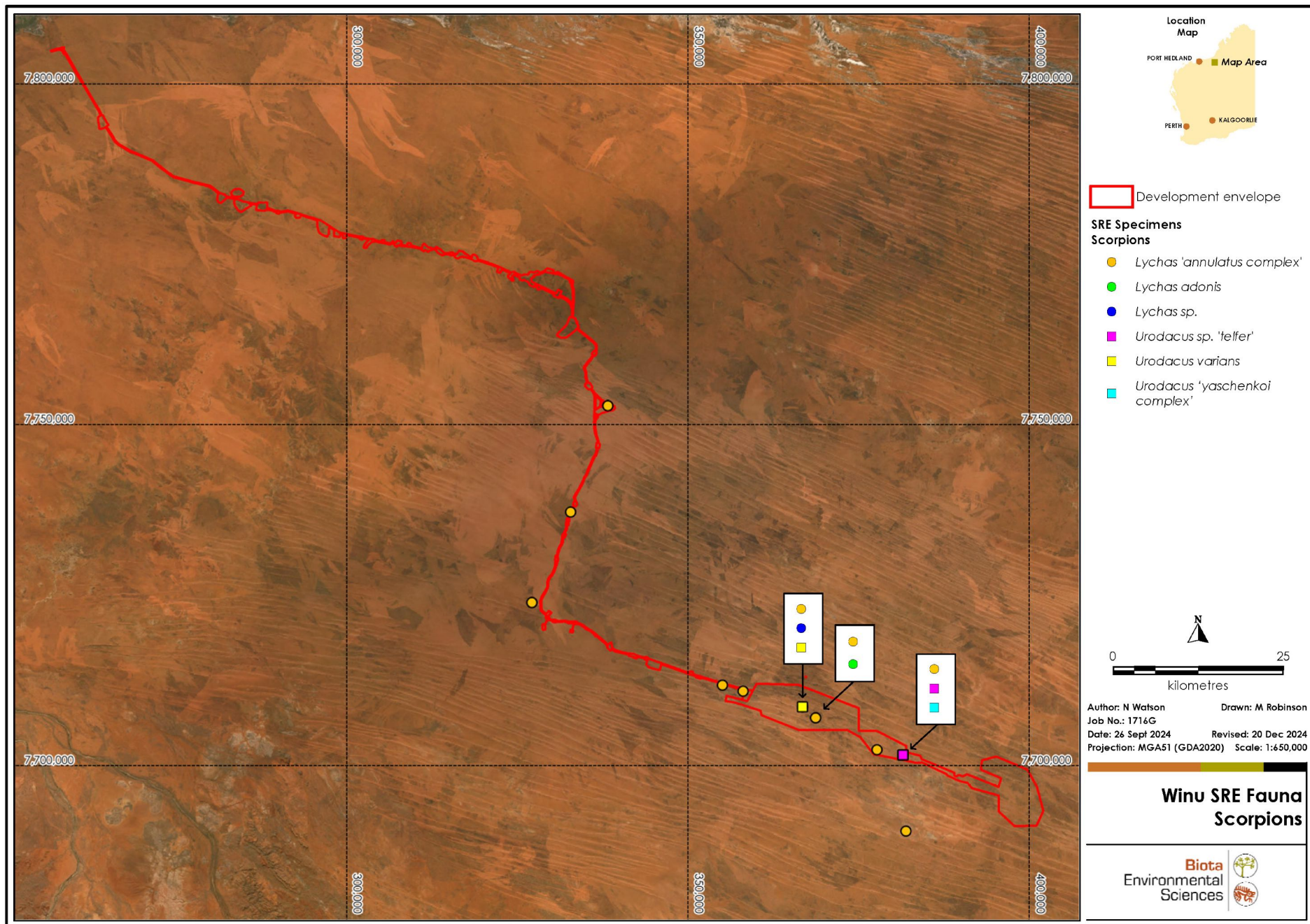


Figure 5.4 Location of scorpion fauna recorded in relation to the Winu DE.

6.0 Discussion

The consolidated SRE sampling undertaken in relation to the Winu DE has comprised seven phases of survey, yielding a total of 18 putative mygalomorph spider species and five scorpion taxa (excluding taxa not identified to genus level). The spider taxa include representatives of four families and the scorpion taxa, two families.

All of the 18 mygalomorph spider species are undescribed molecular species. This is not a surprising result, given the paucity of sampling for terrestrial invertebrate fauna in the Great Sandy Desert region. Molecular analysis revealed that three of these 18 species have been recorded over 240 km away and are therefore not considered likely to be SREs.

Seven of the remaining 15 potential SRE taxa have only been recorded within the Winu DE (see Table 5.4) and all seven taxa are recorded from single sites. This makes any discussion on the distribution of the fauna or, therefore, the risk of small-scale spatial restrictions, challenging. What we can say is that these species are from genera known to have SRE representatives, and so the most conservative assessment would classify these taxa as potential SRE fauna, despite the lack of additional records. However, all seven species were recorded from Shrub and spinifex on sandplain (eight species) and Inland sand dune habitat (one species), and therefore were not collected from restricted or isolated habitats.

Two of the five scorpion taxa recorded from Winu are potential SREs:

- *Urodacus* sp. 'Telfer' – known from outside of Winu but only from an area south of Telfer; and
- *Urodacus* 'yaschenkoi species complex' - the Winu specimens did not show affinity to any reference specimens within the complex.

Both taxa were recorded from Inland sand dune habitat.

The habitats of the Winu DE generally do not have significant potential to support SRE fauna. The majority of the DE is represented by Shrub and spinifex on sandplain habitat (72%), followed by Inland sand dune (13%) and Gravelly lateritic rises (13%); none of which are isolated landforms or host microhabitats conducive to short-range endemism. These widely-connected habitats have no obvious geographic barriers to dispersal which could restrict gene flow and promote short range endemism or contain elevated habitat isolates that could represent long-term refugia (EPA 2016). In addition, the DE generally lacks the type of drainage features which typically give rise to sheltered microhabitats which have greater moisture retention than the surrounding areas and can support SRE fauna.

Looking at the distribution of the documented assemblage: of the four mygalomorph families recorded, three were only recorded to the east of the MIA, including two only recorded outside the DE, south of Rimfire. Based on field observations, this likely coincides with the higher clay content of the soils in that area. The three families recorded east of the MIA (Barychelidae, Halonoproctidae and Idiopidae) are generally found in soils with higher clay content, likely coinciding with the soil landscape B30 unit (Agriculture Western Australia 1967) shown in Figure 4.1. Based on the premise that "*Habitat isolates are more likely to yield SREs than are extensive swathes of contiguous habitat*" (EPA 2016), we consider this soil unit to potentially represent a habitat isolate and therefore to have a higher likelihood of supporting SRE fauna than the rest of the DE.

This unit overlaps less than 1% of the DE and extends outside of the DE south of the Rimfire pipeline corridor. West of the MIA, only spider species belonging to the family Anamidæ were recorded, a family which dominates in the sandier substrates of the arid zone. The likelihood of the species recorded from the RAC and MIA being restricted to very small distributions the size of the RAC and MIA parts of the DE is considered low. It follows that it is highly unlikely that any of these species would be restricted to the DE and that further survey work would likely extend the known distributions of these species outside of the DE.

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Appendix 1

Molecular Analyses by Helix Molecular Solutions



Helix

Molecular Solutions

School of Animal Biology The University of Western Australia
Hackett Entrance No. 4 Hackett Drive Crawley WA 6009

PO Box 155
Leederville WA 6903

t: [08] 6488 4509

f: [08] 6488 1029

abn: 32 133 230 243

w: www.helixsolutions.com.au

18 July 2019

Penny Brooshooft
Senior Zoologist
Biota Environmental Sciences Pty Ltd
Level 1, 228 Carr Place
Leederville WA 6007

Re. Helix Job 577 - Report on the molecular systematics of the mygalomorph and scorpion specimens from Winu.

Dear Penny,

Following is a summary of the results of the invertebrate molecular investigation we have completed for the Winu Fauna survey. We detected six species of mygalomorphae, none of which have been previously detected, as well as four species of scorpion, all of which have been previously detected based on the material available for comparison. Two spider specimens provided ambiguous results, and require further investigation. One species of scorpion detected may represent more than a single taxon and requires further investigation for taxonomic resolution. Results suggest that amongst the twenty-one successfully sequenced spider specimens, one belonged to a previously unrecorded species of *Idiommata* (family Barychelidae), fifteen specimens belong to a distinct previously unrecorded species of *Kwonkan* (family Nemesiidae), one belongs to a distinct species of Nemesiidae not previously recorded, however statistical support for the phylogenetic placement of this specimen was low so we are unable to assign it to a genus with the data available, three specimens belong to three distinct species of *Aname* (family Nemesiidae) none of which have been previously recorded. Results indicated that one specimen did not belong to the mygalomorphae, instead the family placement remains uncertain, beyond the identification that it is an Araneomorphae. We were unable to obtain a good quality sequence from one specimen, and therefore the placement of this suspected nemesiid specimen remains unresolved. Amongst the eight scorpion specimens, four are thought to belong to the widely distributed species *Lychas annulatus* (family Buthidae), although they are spread between two highly divergent clades that require further taxonomic resolution. The remaining four scorpion specimens belong to three distinct species of *Urodacus* (family Urodacidae).

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Zoë Hamilton, Dr. Terrie Finston and Yvette Hitchen
Helix Molecular Solutions



Background and Objective

The infraorder of Arachnida, Mygalomorphae, includes trapdoor spiders and their kin, and they are frequently identified as short-range endemics (SREs) (e.g. Harvey *et al.*, 2011; Castalanelli *et al.*, 2014). Identification of species has traditionally been performed using morphological techniques, however, only males can be used in identification, as both females and juveniles lack the diagnostic characters used in identification, and furthermore there is a large backlog of undescribed taxa. DNA barcoding with the use of COI mtDNA has become a rapid, objective method aiding mygalomorph species identifications and their distributions, and is recognised as providing important information that regulatory authorities can use to assess environmental impacts of large-scale developments (Harvey *et al.*, 2008; Environmental Protection Authority, 2009; Castalanelli *et al.*, 2014). Extensive molecular work has been conducted on the trap-door spider fauna of Western Australia (Helix, 2009a & b, 2010, 2011a - l, 2012a - i, 2013a & b, 2014a - d, 2015a - e, 2018, 2019). The resulting dataset provides a molecular framework that can be used to provide regional context for localised sampling.

Twenty-two specimens of invertebrate fauna belonging to two families of mygalomorph spiders (Araneae: Mygalomorphae: (Barychelidae and Nemesiidae), and eight specimens belonging to two scorpion families (Scorpionida: Buthidae & Urodacidae) from the Winu survey area in the Little Sandy Desert were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI). The twenty-nine successful resulting molecular sequences were then assessed to determine the number of taxa present and compare these results to those sequences publically available on GenBank, as well as those already in Helix's database for context.

Executive summary

- Twenty-two specimens of mygalomorph spiders from the Winu survey area were sequenced and assessed for variation at the COI mtDNA gene. The molecular data were then placed within an existing molecular taxonomic framework for each family, using COI mtDNA sequences from GenBank, and mygalomorph COI sequences in the Helix database;
- Eight scorpion (Scorpionida) specimens belonging to two families (Buthidae and Urodacidae) from the Winu survey area, in the Little Sandy Desert were sequenced and assessed for variation at the COI mtDNA gene. The molecular data were then placed within an existing molecular taxonomic framework for each family, using COI mtDNA scorpions sequences from GenBank, and COI sequences in the Helix database;
- Three families (Barychelidae, Nemesiidae, and family uncertain) were amongst the twenty-one successfully sequenced spider specimens. Two of these families (Barychelidae & Nemesiidae) were mygalomorphae. Thirteen haplotypes were amongst the twenty successfully sequenced mygalomorphae specimens, with three haplotype shared amongst eleven individuals;
- Two divergent clades of buthid (Buthidae) scorpions were recorded amongst the four specimens. Both clades are currently recognised as *Lychas annulatus*, however we suspect more than a single taxon may exist, due to the observed patterns of phylogenetic structuring over geographical distances;
- Three species (Urodacidae) of *Urodacus* were amongst the four specimens, with one haplotype shared between two specimens.

Methods

Twenty-two spider specimens from eight sampling locations (Table 1) were sequenced for variation at the cytochrome oxidase subunit I gene (COI) using primers LCOI & HCO2 (Folmer *et al.*, 1994). For fifteen of these specimens, these universal COI primers failed to amplify a DNA fragment, therefore specially-designed primers (NF1 & NR1) from Y. Hitchen (unpublished data) were used. The resulting twenty mygalomorph sequences comprised twelve haplotypes (Table 2).

Eight scorpion specimens from six sampling locations (Table 1) from two families (Buthidae and Urodacidae) were sequenced for variation at the cytochrome oxidase subunit I

gene (COI) using primers LCOI & HCO2 (Folmer *et al.*, 1994). The eight scorpion sequences comprised six haplotypes (Table 2).

The sequences from the total twenty-nine successfully sequenced invertebrate individuals (COI) were edited using Geneious version 6.1.8 software (<https://www.geneious.com>) performed within MEGA version 5.05 (Tamura *et al.*, 2011) using the built-in alignment tool using CLUSTAL W (Thompson *et al.*, 1994) using default parameters. DNA nucleotide sequences were translated into protein sequences to ensure that the amplified sequences corresponded to the target mtDNA. The translated protein sequences were then checked for the presence of stop codons, to ensure that pseudogenes hadn't been amplified. Pseudogenes have a DNA sequence that is similar to the functional gene (e.g. COI) however, they do not code for a functioning protein despite the shared ancestry with the functional gene. The presence of pseudogenes can complicate molecular analyses, producing odd results. DNA sequences were translated into proteins with ExPASy using the invertebrate genetic code. All sequences analysed were of high quality with no evidence of heterogeneous peaks. All resulting sequences were 'BLAST'ed (Basic Local Alignment Search Tool) with the NCBI (National Centre for Biotechnology Information). This program compares DNA nucleotide sequences with a library of sequences and identifies sequences within the database that resemble the query sequences above a certain threshold. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotides different between sequences). To account for polymorphism within lineages, the net genetic diversity of Nei (1987) was calculated to give a 'corrected' distance between lineages.

For phylogenetic analysis, likelihood ratio tests using the Bayesian Information Criterion were calculated in MEGA 7.0 (Kumar *et al.*, 2016) to determine the best-fit model of evolution. The phylogenetic analyses were calculated in MEGA 7.0 (Kumar *et al.*, 2016) using maximum likelihood (ML) with 1000 bootstrap replicates, based on the genetic distances with the best-fit model of evolution calculated for each family. The tree was rooted using two outgroups, *Centruroides vittatus* (EU404114), and *Mesobuthus martensii* (JF700146) obtained from GenBank.

For the Barychelidae, the best model of evolution was the General Time Reversible model with gamma distribution (GTR+G), with the parameter for gamma distribution of 0.24. For the Nemesiidae, the best model of evolution was the General Time Reversible model with gamma distribution and invariant sites (GTR+G+I), with the parameter for gamma distribution of 0.71.

For both scorpion families (Buthidae and Urodacidae), the best model of evolution was the General Time Reversible model with gamma distribution and invariant sites (GTR+G+I). For the Buthidae the parameter for gamma distribution was 0.93, for the Urodacidae the parameter for the gamma distribution was 0.87.

The phylogenetic analysis were performed separately for each family, and included the representative haplotypes for the eight specimens from the survey area, as well as a total of seventy-five reference specimens obtained from both Helix's and from GenBank (Appendix 1).

For the Nemesiidae a reduced dataset was secondarily analysed for simplification of the phylogenetic tree, due to the large number of samples examined. However, the full dataset was examined for relationships to reference specimens.

Results

Mygalomorphae – family Barychelidae

The single barychelid specimen from Winu was analysed along with twelve reference specimens from the Helix database (n=6) and GenBank (n=6). Based on phylogenetic analyses, the barychelid Winu specimen does not show affinity to any previously sequenced specimens available for comparison (Table 3). According to molecular data the Winu barychelid represents a previously unrecorded species *Idiommata* sp BBT_B39 (Figure 1).

Phylogenetic Analyses

A 686 base-pair (bp) fragment of COI was isolated for the single barychelid specimen from Winu.

Differentiation within and between lineages

The Winu specimen showed 7.7 % sequence divergence from the nearest relative, BBS_B38_OY27, an *Idiommata* from the Helix database collected 60km SW of Onslow.

Mygalomorphae – family Nemesiidae

The nineteen nemesiid specimens from Winu were analysed along with one hundred and ten reference specimens from the Helix database (n=62) and GenBank (n=48). Amongst the nineteen nemesiid Winu specimens, fifteen individuals (Table 4) belong to the newly recorded species *Kwonkan* sp NSD_N151 (Figure 2), one specimen (PC15) belongs to the newly recorded species *Genus?* sp NRC_N150. The remaining three specimens each represent a new distinct *Aname* species, not previously recorded. One specimen (PC18) belongs to the newly recorded species *Aname* sp NRZ_N147, another (PC16) to the new species *Aname* sp. NSA_N148, and the last specimen (PC26) to the new species *Aname* sp NSB_N149. Amongst the nineteen nemesiid specimens from Winu, eleven haplotypes existed, one haplotype (PC28) was shared amongst six individuals, another (PC29) was shared amongst three individuals, and one (PC12) was shared between two individuals.

Phylogenetic Analyses

A 686 base-pair (bp) fragment of COI was isolated for the three of the nemesiid specimens from Winu. For the remaining sixteen specimens, a 422 bp fragment of COI was isolated and analysed, the result of using the specially-designed primers (NF1 & NR1) from Y. Hitchen (unpublished data).

Differentiation within and between lineages

The species *Kwonkan* sp NSD_N151 (n=14) (table 4) showed up to 2.5 % intraspecific variation amongst individuals. The closest relative to the species, based on genetic distance, was a specimen from GenBank (KJ45281.1) that showed 11.0 % sequence divergence from the Winu *Kwonkan* sp NSD_N151 (Table 4).

The species *Genus ?* sp. NRC_N150 (n= 1; PC15) was represented by a single specimen and hence showed no intraspecific sequence divergence. The closest relative, based on genetic distance, to this newly recorded species was also collected from Winu (*Kwonkan* sp NSD_N151) with 12.3 % sequence divergence (Table 4). The phylogenetic placement of this specimen (PC15), even to genus level, is unresolved due to the poor diagnostic support (bootstrap support on tree nodes, Figure 2). Despite the poor resolution, it still did not align with more than 1000 references specimens of Nemesiidae in the Helix database, nor any of the nemesiids on GenBank, and is therefore likely to represent a new taxon. Further resolution may be possible with additional genes.

The newly recorded species *Aname* sp NRZ_N147, (n=1; PC18) was also represented by a single specimen and hence showed no intraspecific sequence divergence. The closest relative, based on genetic distance, showed 13.7 % sequence divergence and was a specimen from the Helix database (NCU_N110_O211) collected 21 km E of Caiguna (Table 4).

The newly recorded species *Aname* sp NSA_N148, (n=1; PC16) was also represented by a single specimen and hence showed no intraspecific sequence divergence. The closest relative, based on genetic distance, was the Winu species *Aname* sp NSB_N149 with 8.2 % sequence divergence (Table 4). It also showed 8.5 % sequence divergence from an *Aname* specimen obtained from GenBank (KJ745288.1) also registered at the WA Museum (T82304) (Table 4).

The newly recorded species *Aname* sp NSB_N149 (n=1; PC26), was also represented by a single specimen and hence there was no intraspecific sequence divergence. The closest relatives, based on genetic distance, showed 8.2 % sequence divergence was the species *Aname* sp. NSA_N148 (Table 4). It showed 9.9 % sequence divergence from a species of *Aname* from the Helix database (NAZ_N6_AD457) collected 5.5 km W of Cossack (Table 4). The three closest GenBank specimens, based on genetic distance and phylogenetic relationships, were all species of *Aname* (KJ745494 (WAM T98900) at 10.7%, KJ745231 (WAM T74238) at 11.0 % and KJ45288 (WAM T82304) at 11.2 % divergence).

Family undetermined

A single specimen (PC11), submitted to Helix as an individual of Nemesiidae, did not align with other mygalmorphae specimens in the Helix and GenBank database. Instead a 'megablast' search places it within the Araneomorphae. Their family assignment is unresolved as numerous identity assignments were found including the families Deinopidae, and Mesysmaucheniidae, (Appendix 2).

Scorpionida – family Buthidae

Over 40 scorpion species described in Australia are traditionally organized into four families: Buthidae, Bothriuridae, Urodacidae and Homuridae (Luna-Ramirez et al., 2017).

The Buthidae are the largest family of scorpions with 1053 species known under 92 genera (Rein, 2015). Few molecular investigations of phylogenetic relationships in the family Buthidae are available (Gantenbein et al., 2000; 2003; Fet et al., 2003; Gantenbein & Lariagadèr, 2003; Mirshamsi et al., 2010; Sousa et al., 2010, 2011; Suranse et al., 2017). Nevertheless, all these studies agree that morpho-taxonomy has limitations in differentiating and defining species boundaries, with findings that several currently recognized species are species groups comprising undescribed taxa. Morphological variability in buthids within taxa, along with morphological similarity between taxa, has led to taxonomic confusion and underscores the value of the inclusion of molecular data for species delineation in scorpions (Yamashita & Rhoads, 2013).

Reference specimens and outgroups

Three haplotypes were among the four sequenced specimens from the Winu study area, one of which was shared amongst two individuals. These sequences were analysed along with fifty-five reference scorpion specimens from GenBank (n= 51) and the Helix database (n= 4) from the family Buthidae. Five representative specimens from five additional scorpion families were used at outgroups in the analysis.

Phylogenetic Analyses

A 686 base-pair (bp) fragment of COI was isolated for all of the four specimens. Because multiple specimens shared identical DNA sequences (haplotypes), the data set was reduced to include only unique haplotypes. Of the four specimens, three had unique haplotypes. Analyses revealed two distinct and strongly supported clades amongst the Winu specimens (Figure 3). These clades (A & B) had a mean divergence of 6.2 % between them. Mean divergences within each lineage were 0.0 % (0.0 % to 0.0 % - clade A) and 4.3 % (0.4 % - 8.6 % - clade B) (Table 6). The closest relative, based on molecular data, for the four buthid specimens from Winu were specimens of *Lychas annulatus* from the Helix databases collected also from the Little Sandy Desert, approximately 40 km NW of the Winu collections (Table 7). Dr. Joel Huey (WA Museum) was previously consulted for assistance with species identification for these *L. annulatus* specimens. Analyses performed by Dr Joel Huey with his more extensive collection of

sequences, not yet publically available (Helix, 2018), placed the *Helix* specimens (NN) in two divergent clades along with specimens identified as *Lychas annulatus* by Lorenzo Prendini (American Museum of Natural History). This species is also recognised as *Hemilychas alexandrinus*, which according to the Atlas of Living Australia has a large distributional range across the arid zone of Australia.

Differentiation within and between lineages

Based on genetic distance of the specimens available for comparison, clade A shows no intraspecific divergence, whilst clade B shows up to 8.6 % intraspecific sequence divergence. The pattern of differentiation amongst specimens of *L. annulatus* does not follow an isolation by distance model. Rather, clade A shows no differentiation between specimens over 60 km (PC06 & NN03), whilst specimens less than 4 km distance apart (PC04 & PC06) show 7.6 % sequence divergence from one another. These phylogeographic patterns of differentiation suggest two distinct lineages, and these may well represent separate taxa, they will require further investigation for taxonomic resolution.

The closest relative to the Winu *Lychas annulatus* clade A specimens (PC06, PC02), based on genetic distance, were specimens from the *Helix* database collected 60 km NW, also from the Little Sandy Desert, one of which shared the same haplotype (Table 6). The next closest relative, were those from clade B with 7.6 % to 8.6 % divergence collected from the Winu study area and 60 km to the NW. The closest relative obtained from GenBank was '*Isometrus* sp.' (MF422313.1) that showed 13.0 % sequence divergence.

The closest relative to the Winu *Lychas annulatus* clade B specimens was a specimen from the same clade collected (NN04) that showed 2.6 % sequence divergence (Table 6). The next closest relatives were those from clade A with 7.6 % to 8.6 % sequence divergence. The closest relative obtained from GenBank specimen was a *Lychas mucronatus* (JN0181153.1) that showed 12.6 % sequence divergence.

Scorpionida – family Urodacidae

The Urodacidae is an Australian endemic family found across the continent, except on the south-eastern seaboard. It was first described by Koch (1977) and under the current classification includes two genera: *Urodacus* and the recently described troglobitic *Aops* (Volschenk & Prendini, 2008). The genus *Urodacus* is endemic in Australia, currently 22 valid species are recognised, although many more are known (Volschenk *et al.*, 2000; Volschenk *et al.*, 2010; Volschenk *et al.*, 2012; Luna-Ramirez *et al.*, 2017)

Reference specimens and outgroups

For analyses conducted by Helix, the four specimens from Winu were analysed along with 34 reference specimens from GenBank, representing eleven families of Scorpionida for context. Amongst the four Winu specimens, three haplotypes existed, with one haplotypes shared amongst two individuals (PC07 & PC08).

Phylogenetic Analyses

Phylogenetic analyses using available GenBank sequences as references placed the four suspected Winu urodacid specimens within the family Urodacidae. The resulting three distinct urodacid lineages show very little affinity to the *Urodacus planimanus* species (Figure 4). As there is a paucity COI urodacid sequences on GenBank, and in the *Helix* database, Dr Erich Volschenk (Alacran), a urodacid specialist, was consulted to determine whether the three divergent lineages of *Urodacus* could be further identified using sequence data generated from a project between Dr Erich Volschenk and the WA museum. Dr Erich Volschenk confirmed that the three distinct molecular lineages represent distinct taxonomic species. His framework allowed further identification with PC03 likely to belong to the species *Urodacus varians*. The Winu *U. varians* specimen differed from other *U. varians* (n=2) sequences by 4.9 % and 4.7 % sequence divergence. These reference specimens are from the Gibson Desert which may explain the relatively large divergences. This species is a dune specialist but is rarely collected owing to the remoteness of its habitat. Dr Volschenk has previously collected the species from the Eastern side of the Gibson Desert but other known records are mostly from the eastern

Pilbara and Sandy Desert, along the Canning Stock Route. The SRE status of some *Urodacus*, including this species, is difficult to ascertain, as there are no data on their distribution type. *Urodacus* species often have patchy distributions so whilst the overall distribution appears to be large, the area of occupancy is significantly smaller. It is thought that *U. varians* is likely present in much of central Western Australia where there are extensive dune fields, the habitat it seems to thrive in (Dr Erich Volschenk pers comm 2019).

PC05 appears to be *Urodacus* sp. 'telfer'. It differed from this species (n=1) by only 4.2 % sequence divergence. This is an undescribed species that was first collected from the vicinity of Telfer. It is only known from a handful of adult males (n=3), which are morphologically diagnostic with very enlarged telsons. This specimen is the fourth record of the species, and the first female specimen. Currently this species is only known from the area south of Telfer and is a potential SRE.

Analyses revealed that the remaining two urodacid specimens (PC07 & PC08) showed likeness to the *Urodacus* 'yaschenkoi species complex' (Luna-Ramirez *et al.*, 2017) ranging from 6.8 % to 5.9 % sequence divergence. At least three putative species exist in this complex based on concordant morphological and molecular species delineation (Luna-Ramirez *et al.*, 2017). This scorpion shares a complex diversification history with other Australian arid-adapted fauna. Despite recognition of the species complex, taxonomic revision is still required. The species-complex is 'usually' associated with red dune systems and collectively has a distribution of Central Queensland to WA Goldfields, but also extends north to near Broome. They are formally describes species within this complex including *U. similis* and *U. carinatus*, as well as many more undescribed taxa. Some appear to be widespread, such as *U. similis* and the eastern goldfields type, whilst others (Broome type – which is describe but currently in synonymy) appear to be SREs. As the Winu specimens didn't show close affinity with any of the reference specimens in the data set, it should be regarded as a Potential SRE. Species in this complex are also morphologically distinctive.

Differentiation within and between lineages

The four urodacid Winu specimens were represented by three haplotypes. Amongst these specimens 0.00 to 10.3 % sequence divergence exists (Table 5; Table 8). From the Helix analysis, the closest relative was a *Urodacus planimanus* specimen (WAM T129654) from GenBank (KY295225.1) at 8.3 % sequence divergence (PC05 & KY295225.1) (Table 8).

Conclusions

The mtDNA gene cytochrome oxidase 1 (*COI*) is widely considered to show suitable variation to distinguish species (Hebert *et al.*, 2003a), and the use of this gene can be extremely effective for 'DNA barcoding' in taxa where clear differentiation exists between intra and interspecific levels of divergence (e.g. Hebert *et al.*, 2004a; 2004b). In a comparison of *COI* sequences for over 13,000 pairs of taxa, Hebert *et al.* (2003b) found a mean of 11.1 % sequence divergence between distinct species. Nearly 80 % of these comparisons found that species pairs differed from one another by greater than 8 % sequence divergence. For mygalomorph spiders, the diversity of species in the Pilbara region of Western Australia has been assessed to test the genetic relationships between and within species, and assess molecular results against morphotype designations comparing *COI* sequences for more than 1000 sequences from seven families, (Castalanelli *et al.*, 2014). The majority (92%) of the morphotypes that had been previously recognised based on adult male morphology were recovered using sequence data, showing the utility of barcoding in mygalomorph spiders (Castalanelli *et al.*, 2014).

Despite its merits in barcoding however, a taxon by taxon approach, examining the amount of phylogenetic variation within and between taxa is the most widely accepted method of delineating species and their distributions, especially in areas where rapidly expanding mining operations outpace taxonomic treatment of unresolved taxa.

In summary, we detected a total of six species from two families among the twenty-two mygalomorph specimens and amongst the eight scorpion specimens we suspect five species of

belonging to two families. All six mygale species have not been recorded previously, based on the sequences available for comparison. The five suspected species of scorpions have all been recorded previously.

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Table 1. Spider specimens used in the present study (n=22), and the genetic lineage to which they belong. Coloured shading refers to colour-coding used to highlight species in Figures 1 and 2. Unshaded cells represent samples that failed to sequence.

Biota Code	Helix Code	Family	Genetic Lineage/Taxonomic ID
M20190520.WIN09P-01	PC09	Barychelidae	<i>Idiommata</i> sp. BBT_B39
M20190517.WINSRE03-01	PC10	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190517.WINSRE03-02	PC11	undetermined	not mygale
M20190518.WINSRE03-01	PC12	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190516.WINSRE05-01	PC13	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190516.WINSRE05-02	PC14	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE04-01	PC15	Nemesiidae	Genus ? NRC_N150
M20190518.WINSRE07-01	PC16	Nemesiidae	<i>Aname</i> sp. NSA_N148
M20190518.WINSRE07-02	PC17	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE07-03	PC18	Nemesiidae	<i>Aname</i> sp. NRZ_N147
M20190518.WINSRE08-01	PC19	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-02	PC20	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-03	PC21	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-04	PC22	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE06-01	PC23	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE06-02	PC24	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE06-03	PC25	Nemesiidae	n/a
M20190513.WINSRE02-01	PC26	Nemesiidae	<i>Aname</i> sp. NSB_N149
M20190513.WINSRE02-02	PC27	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-05	PC28	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-06	PC29	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151
M20190518.WINSRE08-07	PC30	Nemesiidae	<i>Kwonkan</i> sp. NSD_N151

Table 2. Genetic p-distance (below) and the associated standard error (above – blue text) between the twenty mygalomorph individuals, from two families (Barychelidae & Nemesiidae) sequenced from the Winu survey area as shown in Figures 1 and 2. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 2 attached separately as a PDF document due to the size and detail.

Table 3. Genetic p-distance (below) and the associated standard error (above – blue text) between the Winu Barychelidae specimen (in bold text), and all reference specimens, as shown in Figure 1. Colour-coding corresponds to that used in Figures 1. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 3 attached separately as a PDF document due to the size and detail.

Table 4. Genetic p-distance (below) and the associated standard error (above – blue text) between all Nemesiidae mygalomorph haplotypes from Winu (family nemesiidae) and all reference specimens as shown in Figure 2. Colour coding corresponds to Figure 2. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 4 attached separately as a PDF document due to the size and detail.

Table 5. Genetic p-distance (below) and the associated standard error (above – blue text) between the eight scorpion individuals, from two families (Buthidae & Urodacidae) sequenced from the Winu survey area as shown in Figures 3 and 4. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

	PC01	PC02	PC03	PC04	PC05	PC06	PC07	PC08
PC01		0.010	0.014	0.003	0.015	0.010	0.015	0.015
PC02	0.077		0.015	0.010	0.015	0.001	0.015	0.015
PC03	0.162	0.182		0.014	0.012	0.015	0.012	0.012
PC04	0.006	0.076	0.159		0.015	0.010	0.015	0.015
PC05	0.185	0.176	0.103	0.179		0.015	0.011	0.011
PC06	0.076	0.001	0.181	0.074	0.175		0.015	0.015
PC07	0.182	0.179	0.102	0.182	0.089	0.178		0.000
PC08	0.182	0.179	0.102	0.182	0.089	0.178	0.000	

Table 6. Mean within group genetic distances for the two lineages of *Lychas annulatus*.

	Mean genetic distance	s.e.
Clade A	0.000	0.005
Clade B	0.043	0.000

Table 7. Genetic p-distance (below) and the associated standard error (above – blue text) between all buthid scorpion specimens (n=4) (family Buthidae) from Winu, and all reference specimens as shown in Figure 3. Colour coding corresponds to Figure 3. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 7 attached separately as a PDF document due to the size and detail.

Table 8. Genetic p-distance (below) and the associated standard error (above – blue text) between the four *Urodacus* scorpion specimens (family Urodacidae) from Winu, and all reference specimens as shown in Figure 4. Colour coding corresponds to Figure 4. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 8 attached separately as a PDF document due to the size and detail.

Figure 1 attached separately as a PDF document.

Figure 1. Maximum likelihood analysis of Barychelidae COI mtDNA sequences, showing the placement of the Winu barychelid mygalomorphae specimen (in bold text) within the current taxonomic framework of the family Barychelidae. Coloured boxes highlight the species to which the winu specimen belongs. All sequences within 15 % sequence divergence are represented in the tree. 'B' numbers on tree refer to family species based on the 9.5 % species threshold tested in Castalanelli *et al.*, (2014). 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

Figure 2 attached separately as a PDF document due to the size and detail.

Figure 2. Maximum likelihood analysis of the eleven Winu COI mtDNA haplotype sequences, showing the placement of the eleven Winu nemesiid mygalomorphae haplotypes (in bold text) representing nineteen specimens, within the current taxonomic framework of the family Nemesiidae. Coloured boxes highlight the species to which the winu specimens belong. All sequences within 15 % sequence divergence are represented in the tree. 'N' numbers on tree refer to family species based on the 9.5 % species threshold tested in Castalanelli *et al.*, (2014). 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

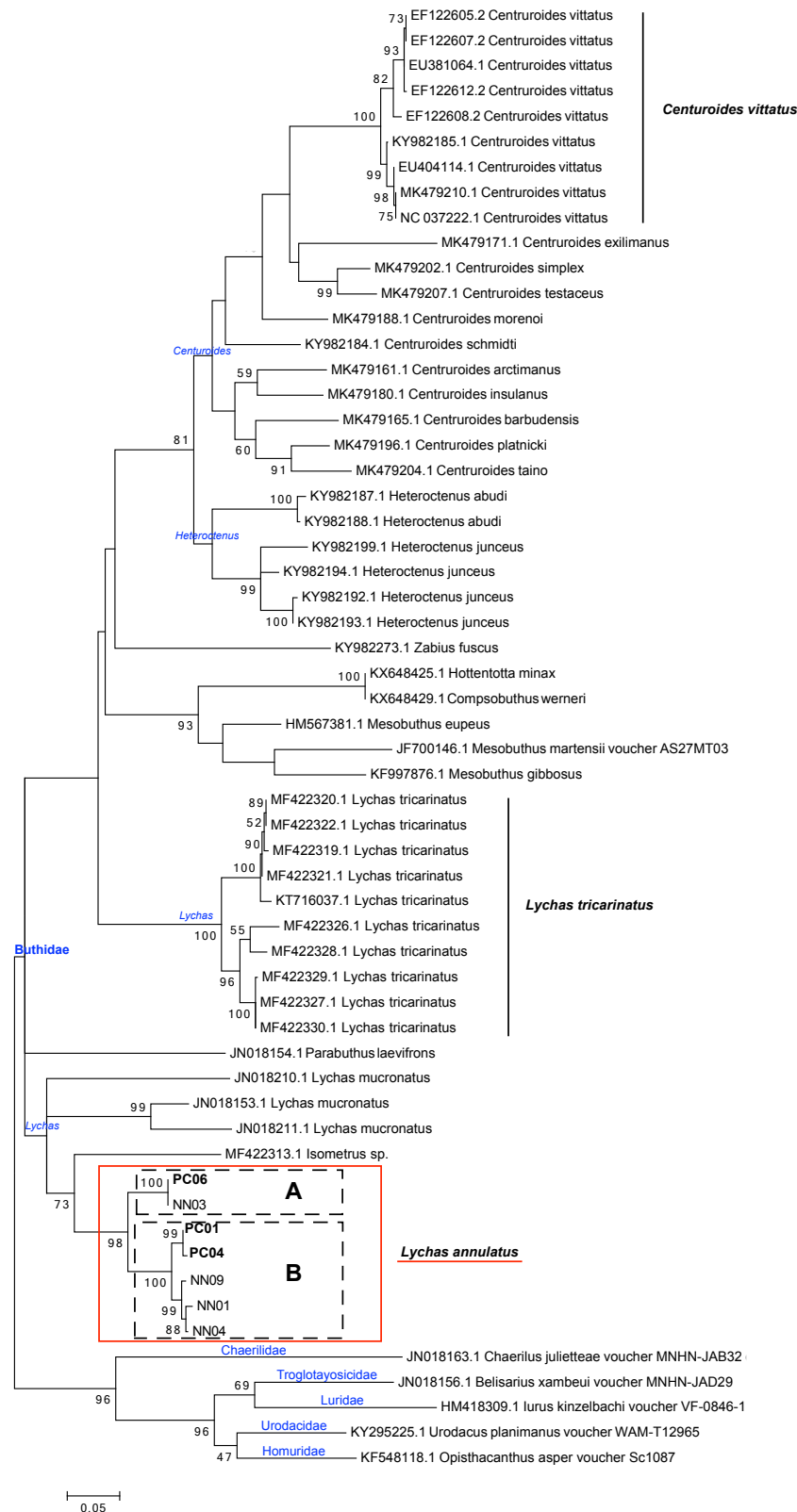


Figure 3. Maximum likelihood analysis of the three buthid COI/mtDNA haplotype sequences, showing the placement of the Winu *Lychas* scorpion specimens (in bold text) within the current taxonomic framework of the family Buthidae. Coloured boxes highlight the species to which the Winu specimens belong. Boxes with dashed lines show distinct lineages. All available sequences within 15 % sequence divergence are represented in the tree. 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

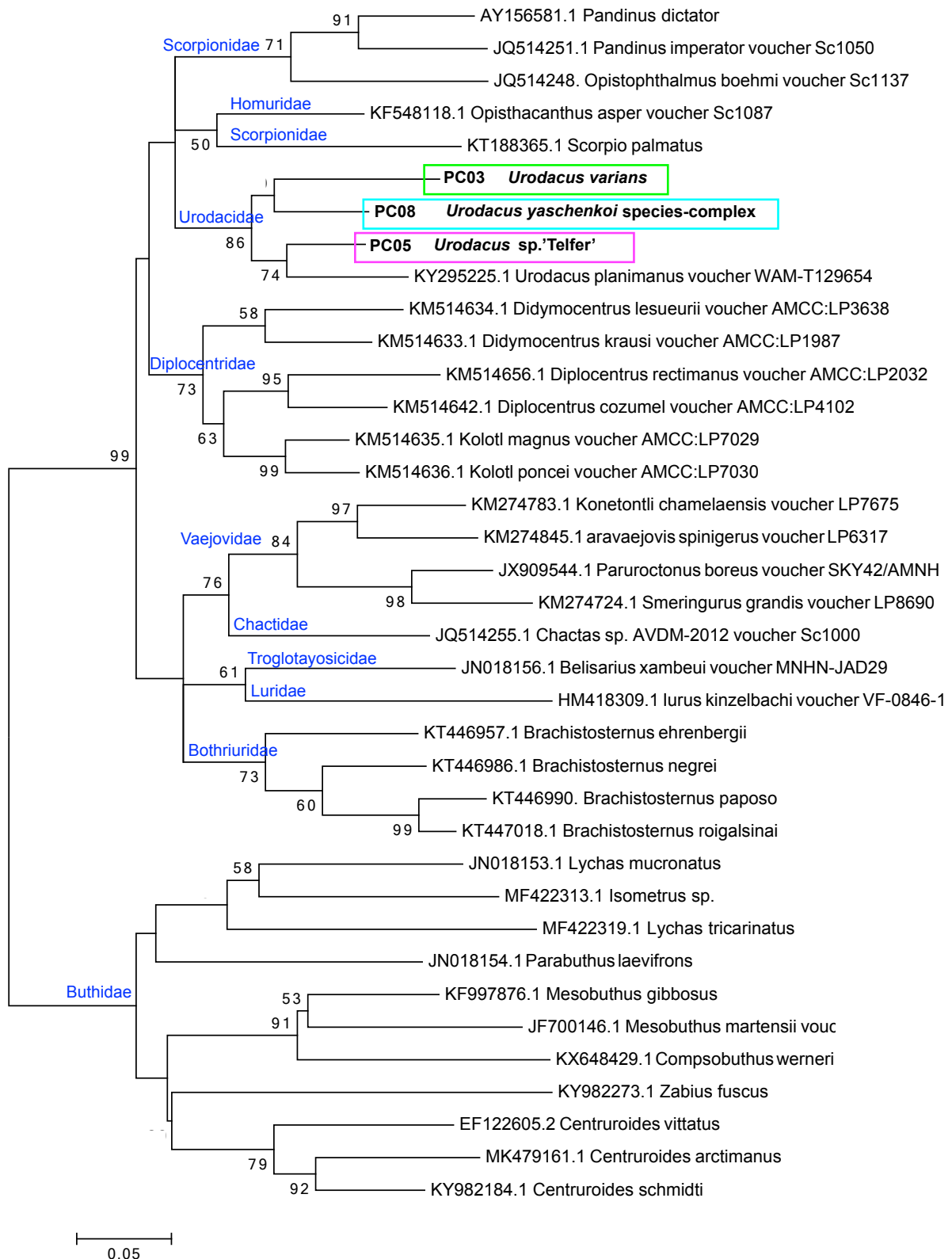


Figure 4. Maximum likelihood analysis of the three urodacid COI mtDNA haplotype sequences, showing the placement of the Winu scorpion specimens (in bold text) within the current taxonomic framework of the family Urodacidae and Scorpionida. Coloured boxes highlight the species to which the Winu specimens belong. All available sequences within 15 % sequence divergence are represented in the tree, as well as family representatives. 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

Appendix 1. Invertebrate reference specimens utilized during analysis in the present study, the source of the data, and the genetic lineage to which they belong.

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
NN01	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN03	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN04	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN09	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
n/a	EF122605.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122607.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122608.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122612.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EU381064.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EU404114.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	HM567381.1	<i>Mesobuthus</i>	<i>eupeus</i>	n/a	GenBank	Buthidae
n/a	JF700146.1	<i>Mesobuthus</i>	<i>martensii</i>	AS27MT03	GenBank	Buthidae
n/a	JN018153.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	JN018154.1	<i>Parabuthus</i>	<i>laevifrons</i>	n/a	GenBank	Buthidae
n/a	JN018210.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	JN018211.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	KF997876.1	<i>Mesobuthus</i>	<i>gibbosus</i>	n/a	GenBank	Buthidae
n/a	KT716037.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	KX648425.1	<i>Hottentotta</i>	<i>minax</i>	n/a	GenBank	Buthidae
n/a	KX648429.1	<i>Compsobuthus</i>	<i>wernerii</i>	n/a	GenBank	Buthidae
n/a	KY982184.1	<i>Centruroides</i>	<i>schmidtii</i>	n/a	GenBank	Buthidae
n/a	KY982185.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	KY982187.1	<i>Heteroctenus</i>	<i>abudi</i>	n/a	GenBank	Buthidae
n/a	KY982188.1	<i>Heteroctenus</i>	<i>abudi</i>	n/a	GenBank	Buthidae
n/a	KY982192.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982193.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982194.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982199.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982273.1	<i>Zabius</i>	<i>fuscus</i>	n/a	GenBank	Buthidae
n/a	MF422313.1	<i>Isometrus</i>	<i>sp.</i>	n/a	GenBank	Buthidae
n/a	MF422319.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422320.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422321.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422322.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422326.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422327.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422328.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422329.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422330.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MK479161.1	<i>Centruroides</i>	<i>arctimanus</i>	n/a	GenBank	Buthidae
n/a	MK479165.1	<i>Centruroides</i>	<i>barbudensis</i>	n/a	GenBank	Buthidae
n/a	MK479171.1	<i>Centruroides</i>	<i>exilimanus</i>	n/a	GenBank	Buthidae
n/a	MK479180.1	<i>Centruroides</i>	<i>insulanus</i>	n/a	GenBank	Buthidae
n/a	MK479188.1	<i>Centruroides</i>	<i>morenoi</i>	n/a	GenBank	Buthidae
n/a	MK479196.1	<i>Centruroides</i>	<i>platnicki</i>	n/a	GenBank	Buthidae
n/a	MK479202.1	<i>Centruroides</i>	<i>simplex</i>	n/a	GenBank	Buthidae
n/a	MK479204.1	<i>Centruroides</i>	<i>taino</i>	n/a	GenBank	Buthidae
n/a	MK479207.1	<i>Centruroides</i>	<i>testaceus</i>	n/a	GenBank	Buthidae
n/a	MK479210.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	NC37222.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	JN018156.1	<i>Belisarius</i>	<i>xambeui</i>	MNHN-JAD29	GenBank	Troglotayosicidae
n/a	KY295225.1	<i>Urodacus</i>	<i>planimanus</i>	WAM-T12965	GenBank	Urodacidae
n/a	JN018163.1	<i>Chaerilus</i>	<i>julietteae</i>	MNHN-JAB32	GenBank	Chaerilidae
n/a	HM418309.1	<i>Iurus</i>	<i>kinzelbachi</i>	VF-0846-1	GenBank	Luridae
n/a	KF548118.1	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae
n/a	KT446990.1	<i>Brachistosternus</i>	<i>paposo</i>	n/a	GenBank	Bothriuridae
n/a	KT447018.1	<i>Brachistosternus</i>	<i>roigalsinai</i>	n/a	GenBank	Bothriuridae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KT446957.1	<i>Brachistosternus</i>	<i>ehrenbergii</i>	n/a	GenBank	Bothriuridae
n/a	KM514656.1	<i>Diplocentrus</i>	<i>rectimanus</i>	AMCC:LP2032	GenBank	Diplocentridae
n/a	KM514642.1	<i>Diplocentrus</i>	<i>cozumel</i>	AMCC:LP4102	GenBank	Diplocentridae
n/a	KT446986.1	<i>Brachistosternus</i>	<i>negrei</i>	n/a	GenBank	Bothriuridae
n/a	KM514634.1	<i>Didymocentrus</i>	<i>lesueurii</i>	AMCC:LP3638	GenBank	Diplocentridae
n/a	KM514633.1	<i>Didymocentrus</i>	<i>krausi</i>	AMCC:LP1987	GenBank	Diplocentridae
n/a	KM514635.1	<i>Kolotl</i>	<i>magnus</i>	AMCC:LP7029	GenBank	Diplocentridae
n/a	KM514636.1	<i>Kolotl</i>	<i>poncei</i>	AMCC:LP7030	GenBank	Diplocentridae
n/a	AY156581.1	<i>Pandinus</i>	<i>dictator</i>	n/a	GenBank	Scorpionidae
n/a	KM274783.1	<i>Konetontli</i>	<i>chamelaensis</i>	LP7675	GenBank	Vaejovidae
n/a	JQ514251.1	<i>Pandinus</i>	<i>imperator</i>	Sc1050	GenBank	Scorpionidae
n/a	JX909544.1	<i>Paruroctonus</i>	<i>boreus</i>	SKY42/AMNH	GenBank	Vaejovidae
n/a	KF548118.1	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae
n/a	JQ514248.1	<i>Opisthophthalmus</i>	<i>boehmi</i>	Sc1137	GenBank	Homuridae
n/a	KT188365.1	<i>Scorpio</i>	<i>palmatatus</i>	n/a	GenBank	Scorpionidae
n/a	JQ514255.1	<i>Chactas</i>	<i>sp.</i>	AVDM-2012	GenBank	Chactidae
n/a	KM274845.1	<i>Paravaejovis</i>	<i>spinigerus</i>	LP6317	GenBank	Vaejovidae
n/a	KM274724.1	<i>Smeringurus</i>	<i>grandis</i>	LP8690	GenBank	Vaejovidae
NA_N1_AG1	n/a	NA	N1	n/a	Helix database	Nemesiidae
NAA_N45_AS38	n/a	NAA	N45	n/a	Helix database	Nemesiidae
NAB_N46_AS41	n/a	NAB	N46	n/a	Helix database	Nemesiidae
NAD_N93_AC10	n/a	NAD	N93	n/a	Helix database	Nemesiidae
NAM_N49_AD14	n/a	NAM	N49	n/a	Helix database	Nemesiidae
NAO_N22_AD328	n/a	NAO	N22	n/a	Helix database	Nemesiidae
NAQ_N5_AD352	n/a	NAQ	N5	n/a	Helix database	Nemesiidae
NAW_N6_AD429	n/a	NAW	N6	n/a	Helix database	Nemesiidae
NAX_N24_AD452	n/a	NAX	N24	n/a	Helix database	Nemesiidae
NAZ_N6_AD457	n/a	NAZ	N6	n/a	Helix database	Nemesiidae
NB_N16_AH8	n/a	NB	N16	n/a	Helix database	Nemesiidae
NBC_N6_AD577	n/a	NBC	N6	n/a	Helix database	Nemesiidae
NBE_N46_AD583	n/a	NBE	N46	n/a	Helix database	Nemesiidae
NBM_N4_AD678	n/a	NBM	N4	n/a	Helix database	Nemesiidae
NBR_N14_AD746	n/a	NBR	N14	n/a	Helix database	Nemesiidae
NBT_N7_AD748	n/a	NBT	N7	n/a	Helix database	Nemesiidae
NBU_N15_AD753	n/a	NBU	N15	n/a	Helix database	Nemesiidae
NBW_N50_AD784	n/a	NBW	N50	n/a	Helix database	Nemesiidae
NCA_N20_AF78	n/a	NCA	N20	n/a	Helix database	Nemesiidae
NCG_N95_I16	n/a	NCG	N95	n/a	Helix database	Nemesiidae
NCU_N110_O211	n/a	NCU	N110	n/a	Helix database	Nemesiidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
NCW_N66_O280	n/a	NCW	N66	n/a	Helix database	Nemesiidae
NCY_N67_O282	n/a	NCY	N67	n/a	Helix database	Nemesiidae
NCZ_N110_O285	n/a	NCZ	N110	n/a	Helix database	Nemesiidae
NDD_N101_O292	n/a	NDD	N101	n/a	Helix database	Nemesiidae
NDK_N94_O333	n/a	NDK	N94	n/a	Helix database	Nemesiidae
NDL_N96_O334	n/a	NDL	N96	n/a	Helix database	Nemesiidae
NEH_N112_BI22	n/a	NEH	N112	n/a	Helix database	Nemesiidae
NEM_N43_DW15	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEM_N43_AT53	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEW_N19_AD381	n/a	NEW	N19	n/a	Helix database	Nemesiidae
NFN_N43_CG5	n/a	NFN	N43	n/a	Helix database	Nemesiidae
NFO_N127_CB26	n/a	NFO	N127	n/a	Helix database	Nemesiidae
NFZ_N122_BV095	n/a	NFZ	N122	n/a	Helix database	Nemesiidae
NGC_N129_CW5	n/a	NGC	N129	n/a	Helix database	Nemesiidae
NGE_N130_CW14	n/a	NGE	N130	n/a	Helix database	Nemesiidae
NGN_N19_DC5	n/a	NGN	N19	n/a	Helix database	Nemesiidae
NGS_N136_DG10	n/a	NGS	N136	n/a	Helix database	Nemesiidae
NGV_N35_DW21	n/a	NGV	N35	n/a	Helix database	Nemesiidae
NIG_N22+N23_ID10	n/a	NIG	N22+N23	n/a	Helix database	Nemesiidae
NK_N36_AD110	n/a	NK	N36	n/a	Helix database	Nemesiidae
NRF_N7_NN11	n/a	NRF	N7	n/a	Helix database	Nemesiidae
NRG_N7_NN15	n/a	NRG	N7	n/a	Helix database	Nemesiidae
NRH_N7_NN16	n/a	NRH	N7	n/a	Helix database	Nemesiidae
NRI_N7_NN17	n/a	NRI	N7	n/a	Helix database	Nemesiidae
NRJ_N7_NN18	n/a	NRJ	N7	n/a	Helix database	Nemesiidae
NRK_N7_NN20	n/a	NRK	N7	n/a	Helix database	Nemesiidae
NRL_N7_NN21	n/a	NRL	N7	n/a	Helix database	Nemesiidae
NRM_N7_NN37	n/a	NRM	N7	n/a	Helix database	Nemesiidae
NRO_N7_NN38	n/a	NRO	N7	n/a	Helix database	Nemesiidae
NRP_N138_NN35	n/a	NRP	N138	n/a	Helix database	Nemesiidae
NRQ_N138_NN36	n/a	NRQ	N138	n/a	Helix database	Nemesiidae
NRW_N144_OU21	n/a	NRW	N144	n/a	Helix database	Nemesiidae
NY_N37_AR64	n/a	NY	N37	n/a	Helix database	Nemesiidae
n/a	JQ772136.1	<i>Aname</i>	sp.	T95404	GenBank	Nemesiidae
n/a	KJ744398.1	<i>Aname</i>	<i>mellosa</i>	T101163	GenBank	Nemesiidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KJ744414.1	<i>Aname</i>	sp.	T102047	GenBank	Nemesiidae
n/a	KJ744623.1	<i>Aname</i>	<i>mellosa</i>	T105871	GenBank	Nemesiidae
n/a	KJ744648.1	<i>Aname</i>	sp.	T107087	GenBank	Nemesiidae
n/a	KJ744649.1	<i>Aname</i>	sp.	T107089	GenBank	Nemesiidae
n/a	KJ744661.1	<i>Aname</i>	<i>mellosa</i>	T107942	GenBank	Nemesiidae
n/a	KJ744662.1	<i>Aname</i>	<i>mellosa</i>	T107945	GenBank	Nemesiidae
n/a	KJ744669.1	<i>Aname</i>	<i>mellosa</i>	T107968	GenBank	Nemesiidae
n/a	KJ744775.1	<i>Aname</i>	<i>mellosa</i>	T113629	GenBank	Nemesiidae
n/a	KJ744785.1	<i>Aname</i>	<i>mellosa</i>	T113642	GenBank	Nemesiidae
n/a	KJ744788.1	<i>Aname</i>	<i>mellosa</i>	T113648	GenBank	Nemesiidae
n/a	KJ744791.1	<i>Aname</i>	<i>mellosa</i>	T113654	GenBank	Nemesiidae
n/a	KJ744803.1	<i>Aname</i>	<i>mellosa</i>	T113666	GenBank	Nemesiidae
n/a	KJ744901.1	<i>Aname</i>	sp.	T118789	GenBank	Nemesiidae
n/a	KJ744902.1	<i>Aname</i>	sp.	T118791	GenBank	Nemesiidae
n/a	KJ744909.1	<i>Aname</i>	sp.	T118805	GenBank	Nemesiidae
n/a	KJ744910.1	<i>Aname</i>	sp.	T118811	GenBank	Nemesiidae
n/a	KJ744911.1	<i>Aname</i>	sp.	T118812	GenBank	Nemesiidae
n/a	KJ744914.1	<i>Aname</i>	sp.	T118818	GenBank	Nemesiidae
n/a	KJ744926.1	<i>Aname</i>	<i>mellosa</i>	T119710	GenBank	Nemesiidae
n/a	KJ744963.1	<i>Kwonkan</i>	sp.	T120001	GenBank	Nemesiidae
n/a	KJ744964.1	<i>Kwonkan</i>	sp.	T120003	GenBank	Nemesiidae
n/a	KJ744975.1	<i>Aname</i>	sp.	T121597	GenBank	Nemesiidae
n/a	KJ744977.1	<i>Aname</i>	<i>mellosa</i>	T122200	GenBank	Nemesiidae
n/a	KJ744982.1	<i>Aname</i>	<i>mellosa</i>	T122207	GenBank	Nemesiidae
n/a	KJ744987.1	<i>Aname</i>	<i>mellosa</i>	T122215	GenBank	Nemesiidae
n/a	KJ744990.1	<i>Aname</i>	<i>mellosa</i>	T122219	GenBank	Nemesiidae
n/a	KJ745117.1	<i>Aname</i>	sp.	T125329	GenBank	Nemesiidae
n/a	KJ745134.1	<i>Aname</i>	<i>mellosa</i>	T126250	GenBank	Nemesiidae
n/a	KJ745143.1	<i>Aname</i>	<i>mellosa</i>	T126259	GenBank	Nemesiidae
n/a	KJ745146.1	<i>Aname</i>	<i>mellosa</i>	T126262	GenBank	Nemesiidae
n/a	KJ745153.1	<i>Aname</i>	<i>mellosa</i>	T126271	GenBank	Nemesiidae
n/a	KJ745155.1	<i>Aname</i>	<i>mellosa</i>	T126273	GenBank	Nemesiidae
n/a	KJ745159.1	<i>Aname</i>	<i>mellosa</i>	T126279	GenBank	Nemesiidae
n/a	KJ745160.1	<i>Aname</i>	<i>mellosa</i>	T126280	GenBank	Nemesiidae
n/a	KJ745168.1	<i>Aname</i>	<i>mellosa</i>	T126296	GenBank	Nemesiidae
n/a	KJ745170.1	<i>Aname</i>	<i>mellosa</i>	T126301	GenBank	Nemesiidae
n/a	KJ745210.1	<i>Kwonkan</i>	sp.	T57563	GenBank	Nemesiidae
n/a	KJ745231.1	<i>Aname</i>	sp.	T74238	GenBank	Nemesiidae
n/a	KJ745232.1	<i>Aname</i>	sp.	T74241	GenBank	Nemesiidae
n/a	KJ745233.1	<i>Aname</i>	sp.	T74247	GenBank	Nemesiidae
n/a	KJ745281.1	<i>Kwonkan</i>	sp.	T78543	GenBank	Nemesiidae
n/a	KJ745287.1	<i>Aname</i>	sp.	T82303	GenBank	Nemesiidae
n/a	KJ745288.1	<i>Aname</i>	sp.	T82304	GenBank	Nemesiidae
n/a	KJ745293.1	<i>Aname</i>	sp.	T82309	GenBank	Nemesiidae
n/a	KJ745375.1	<i>Aname</i>	sp.	T93314	GenBank	Nemesiidae
n/a	KJ745494.1	<i>Aname</i>	sp.	T98900	GenBank	Nemesiidae
NHP_MYG175	n/a	<i>Kwonkan</i>	NHP	n/a	Helix database	Nemesiidae
NHD_MYG127	n/a	<i>Synothele</i>	NHD	n/a	Helix database	Nemesiidae
NHG_MYG227	n/a	<i>Aname</i>	NHG	n/a	Helix database	Nemesiidae
NHQ_MYG250	n/a	<i>Aname</i>	NHQ	n/a	Helix database	Nemesiidae
NGX_MYG182	n/a	<i>Aname</i>	NGX	n/a	Helix database	Nemesiidae
NHF_MYG067	n/a	<i>Aname</i>	NHF	n/a	Helix database	Nemesiidae
NHK_MYG185	n/a	<i>Aname</i>	NHK	n/a	Helix database	Nemesiidae
NHJ_MYG034	n/a	<i>Aname</i>	NHJ	n/a	Helix database	Nemesiidae
n/a	KJ745122.1	<i>Idiommata</i>	sp.	T125335	GenBank	Barychelidae
n/a	KJ745116.1	<i>Idiommata</i>	sp.	T125328	GenBank	Barychelidae
n/a	KJ744575.1	<i>Aureococrypta</i>	sp.	T103910	GenBank	Barychelidae
n/a	KJ745103.1	<i>Idiommata</i>	sp.	T123636	GenBank	Barychelidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KJ745100.1	<i>Idiommata</i>	sp.	T123112	GenBank	Barychelidae
n/a	KJ744660.1	<i>Aureococrypta</i>	sp.	T107502	GenBank	Barychelidae
BBS_B38_OY27	n/a	BBS	B38	n/a	Helix database	Barychelidae
BL_B17_AR106	n/a	BL	B17	n/a	Helix database	Barychelidae
BAQ_B22_O117	n/a	BAQ	B22	n/a	Helix database	Barychelidae
BBK_B19_CB32	n/a	BBK	B19	n/a	Helix database	Barychelidae
BAN_B24_O110	n/a	BAN	B24	n/a	Helix database	Barychelidae
BBM_B19_CB5	n/a	BBM	B19	n/a	Helix database	Barychelidae

Appendix 2. 'megaBLAST' search results for Araneomorph Winu specimen 'PC11'

Query Sample	GenBank ID of reference specimen	Percent Identity (%)
PC11	KY017865.1	88.939
PC11	KP209064.1	88.602
PC11	KY017666.1	87.964
PC11	KY017668.1	87.946
PC11	MF811495.1	88.316
PC11	KX537030.1	88.316
PC11	KX536941.1	88.316
PC11	JF886125.1	88.316
PC11	JF886119.1	88.316
PC11	KY587560.1	88.415
PC11	MF467716.1	88.298
PC11	JN817103.1	87.518
PC11	JN308800.1	88.164
PC11	KY017677.1	87.743
PC11	KP646410.1	88.226
PC11	KP209084.1	88.092
PC11	KP209083.1	88.092
PC11	KP209067.1	88.048
PC11	KP209044.1	88.092
PC11	KP209040.1	88.012
PC11	KY017626.1	88.612
PC11	KM831538.1	87.994
PC11	JF884504.1	87.994
PC11	KY017931.1	87.593
PC11	KY017816.1	87.519
PC11	KY017715.1	87.994
PC11	KP646571.1	88.073
PC11	KP209042.1	87.897
PC11	JN817081.1	87.026
PC11	JF884514.1	87.842
PC11	KM825530.1	87.842
PC11	JN817199.1	87.168
PC11	JF884507.1	87.842
PC11	JF884494.1	87.842
PC11	KY017881.1	87.332
PC11	KP648977.1	87.92
PC11	KU875804.1	87.69
PC11	KX762063.1	87.709
PC11	KM244672.1	86.969
PC11	MH321612.1	87.406
PC11	MG816011.1	87.671
PC11	LC310806.1	87.221
PC11	KY018010.1	87.313
PC11	KY017899.1	87.24
PC11	KY017776.1	87.221
PC11	KY017593.1	87.313
PC11	KP253809.1	87.69
PC11	KF442792.1	87.982
PC11	JF411087.1	87.69
PC11	KY007998.1	87.768
PC11	KY017896.1	87.183
PC11	KM486439.1	87.846
PC11	FJ607577.1	87.221
PC11	MK154252.1	87.538
PC11	KY778930.1	88.144
PC11	KP209090.1	87.595
PC11	KP209089.1	87.634

Query Sample	GenBank ID of reference specimen	Percent Identity (%)
PC11	MF808720.1	87.538
PC11	LC310805.1	87.073
PC11	KY017787.1	87.164
PC11	KM839430.1	87.538
PC11	JN817216.1	86.715
PC11	JN817198.1	86.873
PC11	JF411100.1	87.519
PC11	JN299238.1	87.538
PC11	HQ979347.1	87.557
PC11	FJ525318.1	87.538
PC11	KP271816.1	87.054
PC11	KT174686.1	87.443
PC11	KT174685.1	87.538
PC11	KT174684.1	87.443
PC11	MK154166.1	87.386
PC11	MK154152.1	87.386
PC11	MH321625.1	87.292
PC11	KX537443.1	87.386
PC11	KX536876.1	87.386
PC11	KP209038.1	87.405
PC11	LN887156.1	86.944
PC11	LN887155.1	87.034
PC11	KP656865.1	87.367
PC11	KP645878.1	87.405
PC11	JF411088.1	88.691
PC11	JN309667.1	87.386
PC11	JN309666.1	87.386
PC11	JF884979.1	87.386
PC11	JF884567.1	87.386
PC11	JF884498.1	87.386
PC11	KY778983.1	87.752
PC11	KY018062.1	86.905
PC11	KY017920.1	86.905
PC11	KY017672.1	86.976
PC11	KY017671.1	86.976
PC11	KT174769.1	87.386
PC11	KT174768.1	87.386
PC11	KT174753.1	87.386
PC11	KT174751.1	87.386
PC11	KT174750.1	87.386
PC11	KT174747.1	87.386
PC11	KT174725.1	87.386
PC11	KM825253.1	87.234

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
NN01	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN03	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN04	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN09	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
n/a	EF122605.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122607.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122608.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EF122612.2	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EU381064.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	EU404114.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	HM567381.1	<i>Mesobuthus</i>	<i>eupeus</i>	n/a	GenBank	Buthidae
n/a	JF700146.1	<i>Mesobuthus</i>	<i>martensii</i>	AS27MT03	GenBank	Buthidae
n/a	JN018153.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	JN018154.1	<i>Parabuthus</i>	<i>laevifrons</i>	n/a	GenBank	Buthidae
n/a	JN018210.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	JN018211.1	<i>Lychas</i>	<i>mucronatus</i>	n/a	GenBank	Buthidae
n/a	KF997876.1	<i>Mesobuthus</i>	<i>gibbosus</i>	n/a	GenBank	Buthidae
n/a	KT716037.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	KX648425.1	<i>Hottentotta</i>	<i>minax</i>	n/a	GenBank	Buthidae
n/a	KX648429.1	<i>Compsobuthus</i>	<i>weneri</i>	n/a	GenBank	Buthidae
n/a	KY982184.1	<i>Centruroides</i>	<i>schmidtii</i>	n/a	GenBank	Buthidae
n/a	KY982185.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	KY982187.1	<i>Heteroctenus</i>	<i>abudi</i>	n/a	GenBank	Buthidae
n/a	KY982188.1	<i>Heteroctenus</i>	<i>abudi</i>	n/a	GenBank	Buthidae
n/a	KY982192.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982193.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982194.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae
n/a	KY982199.1	<i>Heteroctenus</i>	<i>junceus</i>	n/a	GenBank	Buthidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KY982273.1	<i>Zabius</i>	<i>fuscus</i>	n/a	GenBank	Buthidae
n/a	MF422313.1	<i>Isometrus</i>	<i>sp.</i>	n/a	GenBank	Buthidae
n/a	MF422319.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422320.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422321.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422322.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422326.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422327.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422328.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422329.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MF422330.1	<i>Lychas</i>	<i>tricarinatus</i>	n/a	GenBank	Buthidae
n/a	MK479161.1	<i>Centruroides</i>	<i>arctimanus</i>	n/a	GenBank	Buthidae
n/a	MK479165.1	<i>Centruroides</i>	<i>barbudensis</i>	n/a	GenBank	Buthidae
n/a	MK479171.1	<i>Centruroides</i>	<i>exilimanus</i>	n/a	GenBank	Buthidae
n/a	MK479180.1	<i>Centruroides</i>	<i>insulanus</i>	n/a	GenBank	Buthidae
n/a	MK479188.1	<i>Centruroides</i>	<i>morenoi</i>	n/a	GenBank	Buthidae
n/a	MK479196.1	<i>Centruroides</i>	<i>platnicki</i>	n/a	GenBank	Buthidae
n/a	MK479202.1	<i>Centruroides</i>	<i>simplex</i>	n/a	GenBank	Buthidae
n/a	MK479204.1	<i>Centruroides</i>	<i>taino</i>	n/a	GenBank	Buthidae
n/a	MK479207.1	<i>Centruroides</i>	<i>testaceus</i>	n/a	GenBank	Buthidae
n/a	MK479210.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	NC37222.1	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	JN018156.1	<i>Belisarius</i>	<i>xambeui</i>	MNHN-JAD29	GenBank	Troglotayosicidae
n/a	KY295225.1	<i>Urodacus</i>	<i>planimanus</i>	WAM-T12965	GenBank	Urodacidae
n/a	JN018163.1	<i>Chaerilus</i>	<i>julietteae</i>	MNHN-JAB32	GenBank	Chaerilidae
n/a	HM418309.1	<i>Iurus</i>	<i>kinzelbachi</i>	VF-0846-1	GenBank	Luridae
n/a	KF548118.1	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae
n/a	KT446990.	<i>Brachistosternus</i>	<i>paposo</i>	n/a	GenBank	Bothriruridae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KT447018.1	<i>Brachistosternus</i>	<i>roigalsinai</i>	n/a	GenBank	Bothriuridae
n/a	KT446957.1	<i>Brachistosternus</i>	<i>ehrenbergii</i>	n/a	GenBank	Bothriuridae
n/a	KM514656.1	<i>Diplocentrus</i>	<i>rectimanus</i>	AMCC:LP2032	GenBank	Diplocentridae
n/a	KM514642.1	<i>Diplocentrus</i>	<i>cozumel</i>	AMCC:LP4102	GenBank	Diplocentridae
n/a	KT446986.1	<i>Brachistosternus</i>	<i>negrei</i>	n/a	GenBank	Bothriuridae
n/a	KM514634.1	<i>Didymocentrus</i>	<i>lesueurii</i>	AMCC:LP3638	GenBank	Diplocentridae
n/a	KM514633.1	<i>Didymocentrus</i>	<i>krausi</i>	AMCC:LP1987	GenBank	Diplocentridae
n/a	KM514635.1	<i>Kolotl</i>	<i>magnus</i>	AMCC:LP7029	GenBank	Diplocentridae
n/a	KM514636.1	<i>Kolotl</i>	<i>poncei</i>	AMCC:LP7030	GenBank	Diplocentridae
n/a	AY156581.1	<i>Pandinus</i>	<i>dictator</i>	n/a	GenBank	Scorpionidae
n/a	KM274783.1	<i>Konetontli</i>	<i>chamelaensis</i>	LP7675	GenBank	Vaejovidae
n/a	JQ514251.1	<i>Pandinus</i>	<i>imperator</i>	Sc1050	GenBank	Scorpionidae
n/a	JX909544.1	<i>Paruroctonus</i>	<i>boreus</i>	SKY42/AMNH	GenBank	Vaejovidae
n/a	KF548118.1	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae
n/a	JQ514248.	<i>Opisthophthalmus</i>	<i>boehmi</i>	Sc1137	GenBank	Homuridae
n/a	KT188365.1	<i>Scorpio</i>	<i>palmatius</i>	n/a	GenBank	Scorpionidae
n/a	JQ514255.1	<i>Chactas</i>	sp.	AVDM-2012	GenBank	Chactidae
n/a	KM274845.1	<i>Paravaejovis</i>	<i>spinigerus</i>	LP6317	GenBank	Vaejovidae
n/a	KM274724.1	<i>Smeringurus</i>	<i>grandis</i>	LP8690	GenBank	Vaejovidae
NA_N1_AG1	n/a	NA	N1	n/a	Helix database	Nemesiidae
NAA_N45_AS38	n/a	NAA	N45	n/a	Helix database	Nemesiidae
NAB_N46_AS41	n/a	NAB	N46	n/a	Helix database	Nemesiidae
NAD_N93_AC10	n/a	NAD	N93	n/a	Helix database	Nemesiidae
NAM_N49_AD14	n/a	NAM	N49	n/a	Helix database	Nemesiidae
NAO_N22_AD328	n/a	NAO	N22	n/a	Helix database	Nemesiidae
NAQ_N5_AD352	n/a	NAQ	N5	n/a	Helix database	Nemesiidae
NAW_N6_AD429	n/a	NAW	N6	n/a	Helix database	Nemesiidae
NAX_N24_AD452	n/a	NAX	N24	n/a	Helix database	Nemesiidae

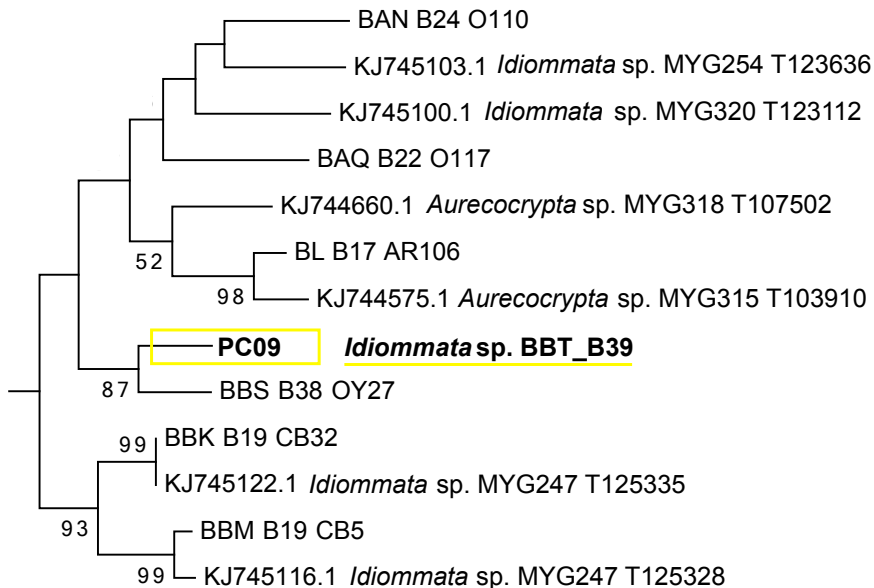
Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
NAZ_N6_AD457	n/a	NAZ	N6	n/a	Helix database	Nemesiidae
NB_N16_AH8	n/a	NB	N16	n/a	Helix database	Nemesiidae
NBC_N6_AD577	n/a	NBC	N6	n/a	Helix database	Nemesiidae
NBE_N46_AD583	n/a	NBE	N46	n/a	Helix database	Nemesiidae
NBM_N4_AD678	n/a	NBM	N4	n/a	Helix database	Nemesiidae
NBR_N14_AD746	n/a	NBR	N14	n/a	Helix database	Nemesiidae
NBT_N7_AD748	n/a	NBT	N7	n/a	Helix database	Nemesiidae
NBU_N15_AD753	n/a	NBU	N15	n/a	Helix database	Nemesiidae
NBW_N50_AD784	n/a	NBW	N50	n/a	Helix database	Nemesiidae
NCA_N20_AF78	n/a	NCA	N20	n/a	Helix database	Nemesiidae
NCG_N95_I16	n/a	NCG	N95	n/a	Helix database	Nemesiidae
NCU_N110_O211	n/a	NCU	N110	n/a	Helix database	Nemesiidae
NCW_N66_O280	n/a	NCW	N66	n/a	Helix database	Nemesiidae
NCY_N67_O282	n/a	NCY	N67	n/a	Helix database	Nemesiidae
NCZ_N110_O285	n/a	NCZ	N110	n/a	Helix database	Nemesiidae
NDD_N101_O292	n/a	NDD	N101	n/a	Helix database	Nemesiidae
NDK_N94_O333	n/a	NDK	N94	n/a	Helix database	Nemesiidae
NDL_N96_O334	n/a	NDL	N96	n/a	Helix database	Nemesiidae
NEH_N112_BI22	n/a	NEH	N112	n/a	Helix database	Nemesiidae
NEM_N43_DW15	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEM_N43_AT53	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEW_N19_AD381	n/a	NEW	N19	n/a	Helix database	Nemesiidae
NFN_N43_CG5	n/a	NFN	N43	n/a	Helix database	Nemesiidae
NFO_N127_CB26	n/a	NFO	N127	n/a	Helix database	Nemesiidae
NFZ_N122_BV095	n/a	NFZ	N122	n/a	Helix database	Nemesiidae
NGC_N129_CW5	n/a	NGC	N129	n/a	Helix database	Nemesiidae
NGE_N130_CW14	n/a	NGE	N130	n/a	Helix database	Nemesiidae
NGN_N19_DC5	n/a	NGN	N19	n/a	Helix database	Nemesiidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
NGS_N136_DG10	n/a	NGS	N136	n/a	Helix database	Nemesiidae
NGV_N35_DW21	n/a	NGV	N35	n/a	Helix database	Nemesiidae
NIG_N22+N23_ID10	n/a	NIG	N22+N23	n/a	Helix database	Nemesiidae
NK_N36_AD110	n/a	NK	N36	n/a	Helix database	Nemesiidae
NRF_N7_NN11	n/a	NRF	N7	n/a	Helix database	Nemesiidae
NRG_N7_NN15	n/a	NRG	N7	n/a	Helix database	Nemesiidae
NRH_N7_NN16	n/a	NRH	N7	n/a	Helix database	Nemesiidae
NRI_N7_NN17	n/a	NRI	N7	n/a	Helix database	Nemesiidae
NRJ_N7_NN18	n/a	NRJ	N7	n/a	Helix database	Nemesiidae
NRK_N7_NN20	n/a	NRK	N7	n/a	Helix database	Nemesiidae
NRL_N7_NN21	n/a	NRL	N7	n/a	Helix database	Nemesiidae
NRM_N7_NN37	n/a	NRM	N7	n/a	Helix database	Nemesiidae
NRO_N7_NN38	n/a	NRO	N7	n/a	Helix database	Nemesiidae
NRP_N138_NN35	n/a	NRP	N138	n/a	Helix database	Nemesiidae
NRQ_N138_NN36	n/a	NRQ	N138	n/a	Helix database	Nemesiidae
NRW_N144_OU21	n/a	NRW	N144	n/a	Helix database	Nemesiidae
NY_N37_AR64	n/a	NY	N37	n/a	Helix database	Nemesiidae
n/a	JQ772136.1	<i>Aname</i>	sp.	T95404	GenBank	Nemesiidae
n/a	KJ744398.1	<i>Aname</i>	<i>mellosa</i>	T101163	GenBank	Nemesiidae
n/a	KJ744414.1	<i>Aname</i>	sp.	T102047	GenBank	Nemesiidae
n/a	KJ744623.1	<i>Aname</i>	<i>mellosa</i>	T105871	GenBank	Nemesiidae
n/a	KJ744648.1	<i>Aname</i>	sp.	T107087	GenBank	Nemesiidae
n/a	KJ744649.1	<i>Aname</i>	sp.	T107089	GenBank	Nemesiidae
n/a	KJ744661.1	<i>Aname</i>	<i>mellosa</i>	T107942	GenBank	Nemesiidae
n/a	KJ744662.1	<i>Aname</i>	<i>mellosa</i>	T107945	GenBank	Nemesiidae
n/a	KJ744669.1	<i>Aname</i>	<i>mellosa</i>	T107968	GenBank	Nemesiidae
n/a	KJ744775.1	<i>Aname</i>	<i>mellosa</i>	T113629	GenBank	Nemesiidae
n/a	KJ744785.1	<i>Aname</i>	<i>mellosa</i>	T113642	GenBank	Nemesiidae

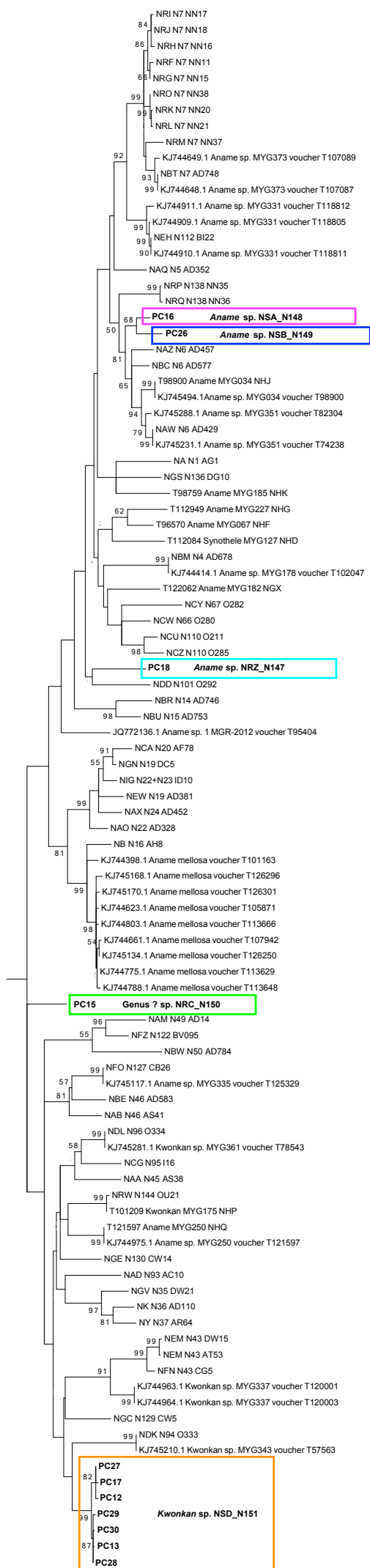
Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KJ744788.1	<i>Aname</i>	<i>mellosa</i>	T113648	GenBank	Nemesiidae
n/a	KJ744791.1	<i>Aname</i>	<i>mellosa</i>	T113654	GenBank	Nemesiidae
n/a	KJ744803.1	<i>Aname</i>	<i>mellosa</i>	T113666	GenBank	Nemesiidae
n/a	KJ744901.1	<i>Aname</i>	sp.	T118789	GenBank	Nemesiidae
n/a	KJ744902.1	<i>Aname</i>	sp.	T118791	GenBank	Nemesiidae
n/a	KJ744909.1	<i>Aname</i>	sp.	T118805	GenBank	Nemesiidae
n/a	KJ744910.1	<i>Aname</i>	sp.	T118811	GenBank	Nemesiidae
n/a	KJ744911.1	<i>Aname</i>	sp.	T118812	GenBank	Nemesiidae
n/a	KJ744914.1	<i>Aname</i>	sp.	T118818	GenBank	Nemesiidae
n/a	KJ744926.1	<i>Aname</i>	<i>mellosa</i>	T119710	GenBank	Nemesiidae
n/a	KJ744963.1	<i>Kwonkan</i>	sp.	T120001	GenBank	Nemesiidae
n/a	KJ744964.1	<i>Kwonkan</i>	sp.	T120003	GenBank	Nemesiidae
n/a	KJ744975.1	<i>Aname</i>	sp.	T121597	GenBank	Nemesiidae
n/a	KJ744977.1	<i>Aname</i>	<i>mellosa</i>	T122200	GenBank	Nemesiidae
n/a	KJ744982.1	<i>Aname</i>	<i>mellosa</i>	T122207	GenBank	Nemesiidae
n/a	KJ744987.1	<i>Aname</i>	<i>mellosa</i>	T122215	GenBank	Nemesiidae
n/a	KJ744990.1	<i>Aname</i>	<i>mellosa</i>	T122219	GenBank	Nemesiidae
n/a	KJ745117.1	<i>Aname</i>	sp.	T125329	GenBank	Nemesiidae
n/a	KJ745134.1	<i>Aname</i>	<i>mellosa</i>	T126250	GenBank	Nemesiidae
n/a	KJ745143.1	<i>Aname</i>	<i>mellosa</i>	T126259	GenBank	Nemesiidae
n/a	KJ745146.1	<i>Aname</i>	<i>mellosa</i>	T126262	GenBank	Nemesiidae
n/a	KJ745153.1	<i>Aname</i>	<i>mellosa</i>	T126271	GenBank	Nemesiidae
n/a	KJ745155.1	<i>Aname</i>	<i>mellosa</i>	T126273	GenBank	Nemesiidae
n/a	KJ745159.1	<i>Aname</i>	<i>mellosa</i>	T126279	GenBank	Nemesiidae
n/a	KJ745160.1	<i>Aname</i>	<i>mellosa</i>	T126280	GenBank	Nemesiidae
n/a	KJ745168.1	<i>Aname</i>	<i>mellosa</i>	T126296	GenBank	Nemesiidae
n/a	KJ745170.1	<i>Aname</i>	<i>mellosa</i>	T126301	GenBank	Nemesiidae
n/a	KJ745210.1	<i>Kwonkan</i>	sp.	T57563	GenBank	Nemesiidae

Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
n/a	KJ745231.1	<i>Aname</i>	sp.	T74238	GenBank	Nemesiidae
n/a	KJ745232.1	<i>Aname</i>	sp.	T74241	GenBank	Nemesiidae
n/a	KJ745233.1	<i>Aname</i>	sp.	T74247	GenBank	Nemesiidae
n/a	KJ745281.1	<i>Kwonkan</i>	sp.	T78543	GenBank	Nemesiidae
n/a	KJ745287.1	<i>Aname</i>	sp.	T82303	GenBank	Nemesiidae
n/a	KJ745288.1	<i>Aname</i>	sp.	T82304	GenBank	Nemesiidae
n/a	KJ745293.1	<i>Aname</i>	sp.	T82309	GenBank	Nemesiidae
n/a	KJ745375.1	<i>Aname</i>	sp.	T93314	GenBank	Nemesiidae
n/a	KJ745494.1	<i>Aname</i>	sp.	T98900	GenBank	Nemesiidae
NHP_MYG175	n/a	<i>Kwonkan</i>	NHP	n/a	Helix database	Nemesiidae
NHD_MYG127	n/a	<i>Synothele</i>	NHD	n/a	Helix database	Nemesiidae
NHG_MYG227	n/a	<i>Aname</i>	NHG	n/a	Helix database	Nemesiidae
NHQ_MYG250	n/a	<i>Aname</i>	NHQ	n/a	Helix database	Nemesiidae
NGX_MYG182	n/a	<i>Aname</i>	NGX	n/a	Helix database	Nemesiidae
NHF_MYG067	n/a	<i>Aname</i>	NHF	n/a	Helix database	Nemesiidae
NHK_MYG185	n/a	<i>Aname</i>	NHK	n/a	Helix database	Nemesiidae
NHJ_MYG034	n/a	<i>Aname</i>	NHJ	n/a	Helix database	Nemesiidae
n/a	KJ745122.1	<i>Idiommata</i>	sp.	T125335	GenBank	Bareychelidae
n/a	KJ745116.1	<i>Idiommata</i>	sp.	T125328	GenBank	Bareychelidae
n/a	KJ744575.1	<i>Aurecocrypta</i>	sp.	T103910	GenBank	Bareychelidae
n/a	KJ745103.1	<i>Idiommata</i>	sp.	T123636	GenBank	Bareychelidae
n/a	KJ745100.1	<i>Idiommata</i>	sp.	T123112	GenBank	Bareychelidae
n/a	KJ744660.1	<i>Aurecocrypta</i>	sp.	T107502	GenBank	Bareychelidae
BBS_B38_OY27	n/a	BBS	B38	n/a	Helix database	Bareychelidae
BL_B17_AR106	n/a	BL	B17	n/a	Helix database	Bareychelidae
BAQ_B22_O117	n/a	BAQ	B22	n/a	Helix database	Bareychelidae
BBK_B19_CB32	n/a	BBK	B19	n/a	Helix database	Bareychelidae
BAN_B24_O110	n/a	BAN	B24	n/a	Helix database	Bareychelidae

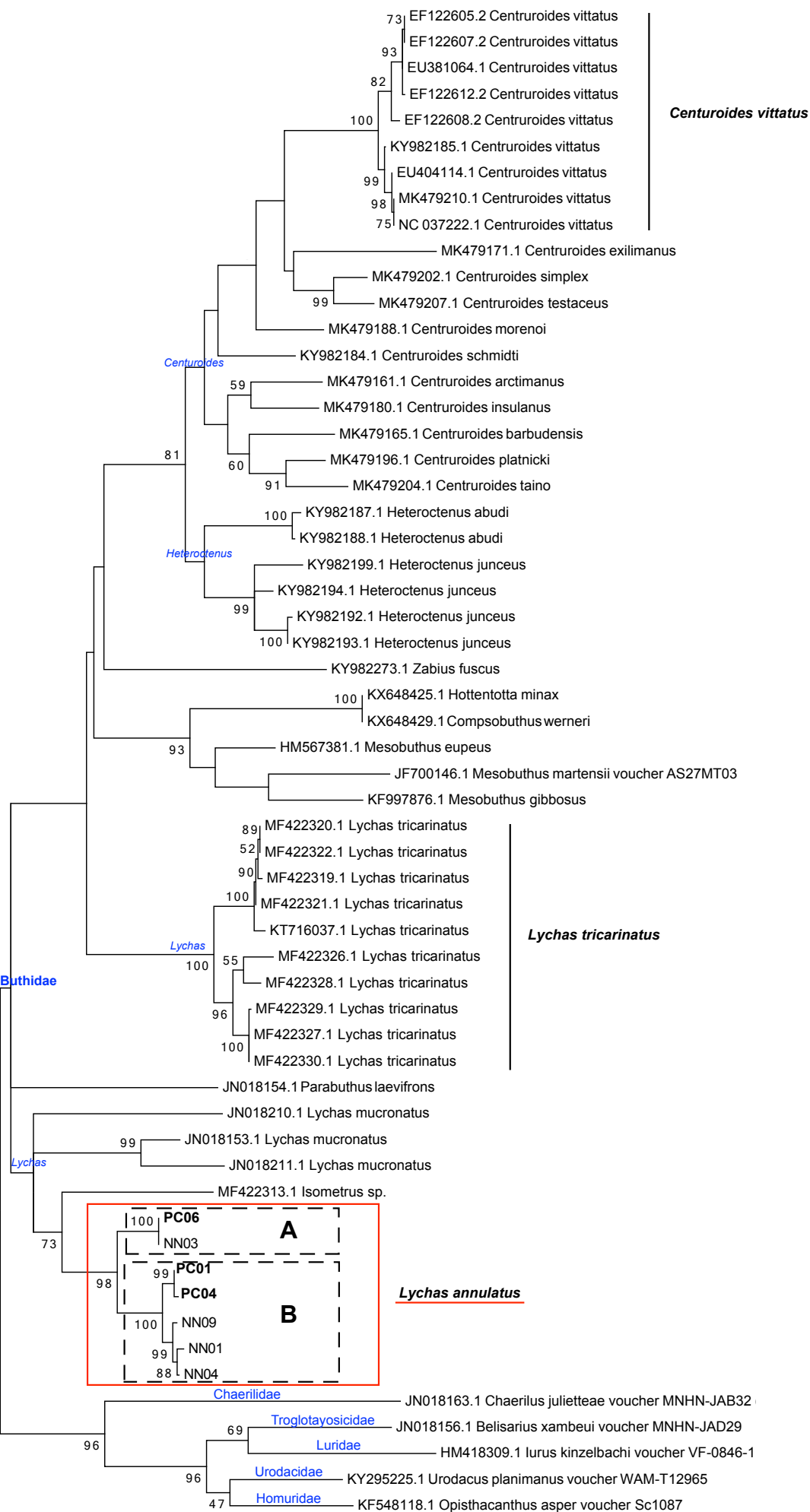
Helix ID	GenBank accession Number	Genus	Species	Voucher	Source	Family
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0.1



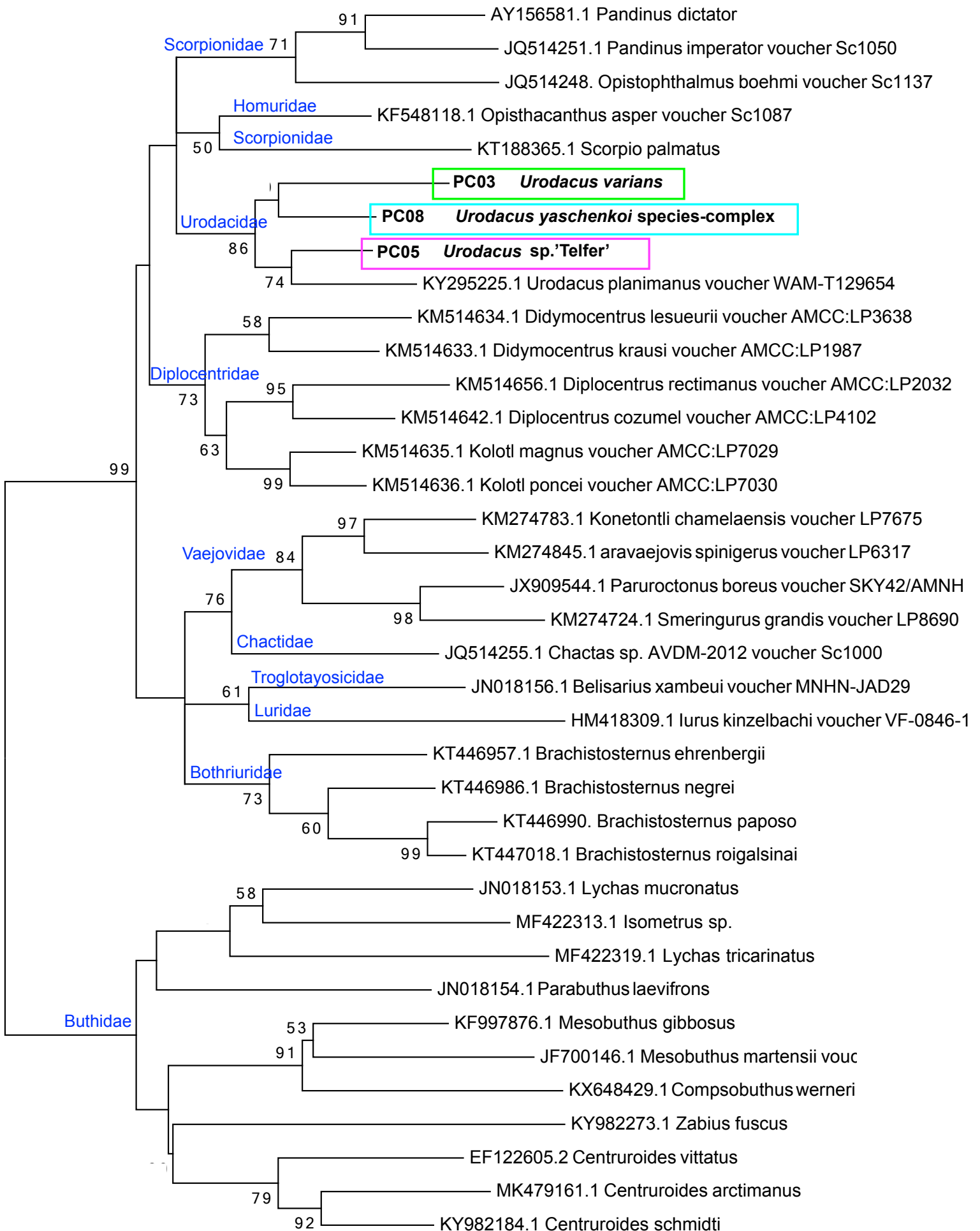
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Centruroides vittatus

Lychas tricarinatus

Lychas annulatus



0.05

	PC16	PC26	PC23	PC24	PC28	PC19	PC20	PC14	PC21	PC29	PC22	PC13	PC10	PC30	PC12	PC17	PC27	PC15	PC18	PC09
PC16		0.013	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.018	0.018	0.020
PC26	0.081		0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.020
PC23	0.178	0.164		0.000	0.000	0.000	0.000	0.000	0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC24	0.178	0.164	0.000		0.000	0.000	0.000	0.000	0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC28	0.178	0.164	0.000	0.000		0.000	0.000	0.000	0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC19	0.178	0.164	0.000	0.000	0.000		0.000	0.000	0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC20	0.178	0.164	0.000	0.000	0.000	0.000		0.000	0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC14	0.178	0.164	0.000	0.000	0.000	0.000	0.000		0.003	0.003	0.003	0.003	0.007	0.002	0.007	0.007	0.006	0.016	0.017	0.019
PC21	0.178	0.169	0.005	0.005	0.005	0.005	0.005	0.005		0.000	0.000	0.005	0.007	0.004	0.007	0.007	0.007	0.016	0.017	0.019
PC29	0.178	0.169	0.005	0.005	0.005	0.005	0.005	0.005	0.000		0.000	0.005	0.007	0.004	0.007	0.007	0.007	0.016	0.017	0.019
PC22	0.178	0.169	0.005	0.005	0.005	0.005	0.005	0.005	0.000	0.000		0.005	0.007	0.004	0.007	0.007	0.007	0.016	0.017	0.019
PC13	0.181	0.162	0.005	0.005	0.005	0.005	0.005	0.005	0.010	0.010	0.010		0.007	0.004	0.007	0.007	0.007	0.016	0.017	0.019
PC10	0.178	0.162	0.019	0.019	0.019	0.019	0.019	0.019	0.024	0.024	0.024	0.024		0.006	0.000	0.005	0.003	0.016	0.017	0.020
PC30	0.181	0.162	0.002	0.002	0.002	0.002	0.002	0.002	0.007	0.007	0.007	0.007	0.017		0.006	0.007	0.006	0.016	0.017	0.019
PC12	0.178	0.162	0.019	0.019	0.019	0.019	0.019	0.019	0.024	0.024	0.024	0.024	0.000	0.017		0.005	0.003	0.016	0.017	0.020
PC17	0.176	0.169	0.019	0.019	0.019	0.019	0.019	0.019	0.024	0.024	0.024	0.019	0.010	0.021	0.010		0.003	0.016	0.017	0.019
PC27	0.178	0.166	0.014	0.014	0.014	0.014	0.014	0.014	0.019	0.019	0.019	0.019	0.005	0.017	0.005	0.005		0.016	0.017	0.019
PC15	0.162	0.159	0.126	0.126	0.126	0.126	0.126	0.126	0.131	0.131	0.131	0.131	0.126	0.126	0.126	0.128	0.128		0.019	0.020
PC18	0.164	0.154	0.138	0.138	0.138	0.138	0.138	0.138	0.143	0.143	0.143	0.133	0.145	0.135	0.145	0.145	0.145	0.176		0.020
PC09	0.202	0.209	0.188	0.188	0.188	0.188	0.188	0.188	0.188	0.188	0.188	0.190	0.202	0.190	0.202	0.195	0.197	0.209	0.221	

		1	2	3	4	5	6	7	8	9
1	PC09		0.013	0.016	0.017	0.016	0.017	0.017	0.016	0.017
2	BBS_B38_OY27	0.077		0.017	0.017	0.017	0.018	0.017	0.017	0.017
3	BL_B17_AR106	0.120	0.123		0.016	0.016	0.017	0.017	0.016	0.017
4	BAQ_B22_O117	0.128	0.128	0.120		0.017	0.017	0.017	0.017	0.017
5	BBK_B19_CB32	0.120	0.123	0.110	0.130		0.017	0.013	0.000	0.013
6	BAN_B24_O110	0.136	0.141	0.136	0.123	0.133		0.017	0.017	0.017
7	BBM_B19_CB5	0.128	0.133	0.125	0.138	0.074	0.128		0.013	0.008
8	KJ745122.1:2-658 <i>Idiommatata</i> sp. MYG247 voucher T125335	0.120	0.123	0.110	0.130	0.000	0.133	0.074		0.013
9	KJ745116.1:2-658 <i>Idiommatata</i> sp. MYG247 voucher T125328	0.130	0.130	0.128	0.133	0.077	0.123	0.023	0.077	
10	KJ744575.1:1-658 <i>Aurecocrypta</i> sp. MYG315 voucher T103910	0.120	0.125	0.049	0.123	0.128	0.146	0.141	0.128	0.143
11	KJ745103.1:2-658 <i>Idiommatata</i> sp. MYG254 voucher T123636	0.133	0.136	0.123	0.130	0.110	0.107	0.130	0.110	0.128
12	KJ745100.1:1-658 <i>Idiommatata</i> sp. MYG320 voucher T123112	0.133	0.115	0.123	0.125	0.143	0.128	0.141	0.143	0.133
13	KJ744660.1:2-658 <i>Aurecocrypta</i> sp. MYG318 voucher T107502	0.148	0.133	0.097	0.113	0.123	0.125	0.148	0.123	0.141

		10	11	12	13
1	PC09	0.016	0.017	0.017	0.018
2	BBS_B38_OY27	0.017	0.017	0.016	0.017
3	BL_B17_AR106	0.011	0.017	0.017	0.015
4	BAQ_B22_O117	0.017	0.017	0.017	0.016
5	BBK_B19_CB32	0.017	0.016	0.018	0.017
6	BAN_B24_O110	0.018	0.016	0.017	0.017
7	BBM_B19_CB5	0.018	0.017	0.018	0.018
8	KJ745122.1:2-658 <i>Idiommatata</i> sp. MYG247 voucher T125335	0.017	0.016	0.018	0.017
9	KJ745116.1:2-658 <i>Idiommatata</i> sp. MYG247 voucher T125328	0.018	0.017	0.017	0.018
10	KJ744575.1:1-658 <i>Aurecocrypta</i> sp. MYG315 voucher T103910		0.017	0.017	0.015
11	KJ745103.1:2-658 <i>Idiommatata</i> sp. MYG254 voucher T123636	0.130		0.017	0.016
12	KJ745100.1:1-658 <i>Idiommatata</i> sp. MYG320 voucher T123112	0.128	0.123		0.017
13	KJ744660.1:2-658 <i>Aurecocrypta</i> sp. MYG318 voucher T107502	0.102	0.110	0.130	

		1	2	3	4	5	6	7	8	9
1	PC12		0.004	0.008	0.008	0.007	0.019	0.017	0.020	0.019
2	PC27	0.005		0.007	0.007	0.006	0.019	0.018	0.020	0.020
3	PC29	0.025	0.019		0.005	0.004	0.019	0.018	0.020	0.020
4	PC13	0.022	0.016	0.008		0.003	0.018	0.017	0.020	0.020
5	PC28	0.019	0.014	0.005	0.003		0.018	0.017	0.020	0.020
6	PC18	0.148	0.148	0.148	0.140	0.142		0.020	0.019	0.019
7	PC15	0.126	0.129	0.129	0.126	0.123	0.175		0.019	0.019
8	PC16	0.181	0.181	0.184	0.184	0.184	0.164	0.159		0.014
9	PC26	0.164	0.170	0.175	0.170	0.170	0.164	0.153	0.082	
10	NA_N1_AG1	0.192	0.197	0.192	0.192	0.195	0.162	0.181	0.156	0.170
11	NAA_N45_AS38	0.137	0.137	0.132	0.137	0.134	0.173	0.145	0.186	0.203
12	NAB_N46_AS41	0.140	0.137	0.137	0.140	0.137	0.148	0.153	0.186	0.181
13	NAD_N93_AC10	0.129	0.129	0.142	0.140	0.137	0.189	0.175	0.211	0.197
14	NAM_N49_AD14	0.159	0.162	0.162	0.162	0.162	0.200	0.181	0.192	0.197
15	NAO_N22_AD328	0.167	0.173	0.170	0.164	0.167	0.167	0.140	0.170	0.162
16	NAQ_N5_AD352	0.178	0.184	0.170	0.173	0.175	0.167	0.173	0.126	0.129
17	NAW_N6_AD429	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110
18	NAX_N24_AD452	0.170	0.170	0.178	0.170	0.173	0.170	0.153	0.162	0.134
19	NAZ_N6_AD457	0.156	0.162	0.162	0.159	0.159	0.145	0.164	0.093	0.099
20	NB_N16_AH8	0.156	0.159	0.164	0.156	0.159	0.153	0.162	0.184	0.192
21	NBC_N6_AD577	0.192	0.195	0.186	0.192	0.192	0.170	0.170	0.099	0.110
22	NBE_N46_AD583	0.145	0.140	0.137	0.140	0.142	0.181	0.151	0.192	0.178
23	NBM_N4_AD678	0.192	0.197	0.184	0.186	0.186	0.164	0.175	0.164	0.167
24	NBR_N14_AD746	0.181	0.181	0.181	0.181	0.181	0.189	0.178	0.167	0.170
25	NBT_N7_AD748	0.167	0.173	0.178	0.173	0.173	0.162	0.167	0.110	0.115
26	NBU_N15_AD753	0.167	0.162	0.162	0.164	0.164	0.153	0.192	0.167	0.159
27	NBW_N50_AD784	0.167	0.164	0.156	0.159	0.159	0.173	0.178	0.167	0.173
28	NCA_N20_AF78	0.186	0.192	0.186	0.184	0.186	0.181	0.151	0.181	0.178

		1	2	3	4	5	6	7	8	9
29	NCG_N95_I16	0.118	0.121	0.121	0.126	0.123	0.184	0.151	0.178	0.184
30	NCU_N110_O211	0.156	0.162	0.156	0.153	0.153	0.137	0.167	0.175	0.151
31	NCW_N66_O280	0.167	0.167	0.178	0.175	0.175	0.164	0.162	0.145	0.145
32	NCY_N67_O282	0.211	0.211	0.205	0.200	0.200	0.164	0.186	0.159	0.156
33	NCZ_N110_O285	0.162	0.167	0.167	0.164	0.164	0.156	0.159	0.181	0.142
34	NDD_N101_O292	0.184	0.181	0.181	0.175	0.178	0.151	0.181	0.153	0.178
35	NDK_N94_O333	0.118	0.118	0.118	0.118	0.115	0.175	0.159	0.186	0.159
36	NDL_N96_O334	0.121	0.118	0.110	0.118	0.115	0.186	0.142	0.192	0.192
37	NEH_N112_BI22	0.167	0.173	0.167	0.164	0.164	0.151	0.178	0.121	0.142
38	NEM_N43_DW15	0.134	0.134	0.140	0.134	0.137	0.167	0.159	0.200	0.195
39	NEM_N43_AT53	0.132	0.132	0.137	0.132	0.134	0.170	0.162	0.203	0.197
40	NEW_N19_AD381	0.181	0.186	0.195	0.186	0.189	0.200	0.156	0.173	0.167
41	NFN_N43_CG5	0.134	0.134	0.140	0.140	0.137	0.178	0.167	0.195	0.208
42	NFO_N127_CB26	0.140	0.142	0.140	0.142	0.140	0.178	0.142	0.197	0.178
43	NFZ_N122_BV095	0.156	0.159	0.162	0.159	0.159	0.184	0.173	0.200	0.192
44	NGC_N129_CW5	0.123	0.118	0.121	0.121	0.118	0.164	0.148	0.184	0.175
45	NGE_N130_CW14	0.121	0.118	0.112	0.115	0.112	0.153	0.132	0.186	0.170
46	NGN_N19_DC5	0.189	0.195	0.195	0.186	0.189	0.184	0.151	0.162	0.151
47	NGS_N136_DG10	0.186	0.184	0.175	0.175	0.178	0.151	0.203	0.151	0.164
48	NGV_N35_DW21	0.134	0.134	0.129	0.134	0.134	0.167	0.170	0.164	0.186
49	NIG_N22+N23_ID10	0.184	0.184	0.178	0.175	0.178	0.192	0.156	0.173	0.175
50	NK_N36_AD110	0.132	0.137	0.132	0.137	0.137	0.178	0.170	0.175	0.178
51	NRF_N7_NN11	0.164	0.170	0.170	0.164	0.164	0.156	0.173	0.112	0.123
52	NRG_N7_NN15	0.164	0.170	0.170	0.164	0.164	0.156	0.164	0.115	0.121
53	NRH_N7_NN16	0.173	0.178	0.178	0.173	0.173	0.170	0.170	0.126	0.132
54	NRI_N7_NN17	0.170	0.175	0.175	0.170	0.170	0.164	0.164	0.121	0.126
55	NRJ_N7_NN18	0.167	0.173	0.173	0.167	0.167	0.167	0.167	0.123	0.129
56	NRK_N7_NN20	0.175	0.181	0.175	0.175	0.175	0.167	0.167	0.107	0.123

		1	2	3	4	5	6	7	8	9
57	NRL_N7_NN21	0.170	0.175	0.170	0.170	0.170	0.162	0.167	0.112	0.118
58	NRM_N7_NN37	0.189	0.195	0.197	0.192	0.192	0.173	0.189	0.126	0.140
59	NRO_N7_NN38	0.173	0.178	0.173	0.173	0.173	0.162	0.173	0.107	0.118
60	NRP_N138_NN35	0.175	0.181	0.178	0.175	0.175	0.173	0.159	0.110	0.121
61	NRQ_N138_NN36	0.175	0.181	0.178	0.175	0.175	0.181	0.167	0.115	0.126
62	NRW_N144_OU21	0.134	0.140	0.142	0.145	0.142	0.186	0.159	0.178	0.173
63	NY_N37_AR64	0.142	0.148	0.145	0.151	0.151	0.186	0.173	0.189	0.181
64	T101209 Kwonkan MYG175 NHP	0.129	0.134	0.140	0.140	0.137	0.181	0.159	0.173	0.173
65	T112084 Synothele MYG127 NHD	0.186	0.189	0.186	0.184	0.184	0.173	0.197	0.142	0.167
66	T112949 Aname MYG227 NHG	0.167	0.173	0.167	0.167	0.170	0.173	0.175	0.142	0.156
67	T121597 Aname MYG250 NHQ	0.121	0.126	0.129	0.134	0.132	0.167	0.151	0.173	0.178
68	T122062 Aname MYG182 NGX	0.175	0.175	0.175	0.170	0.170	0.170	0.173	0.164	0.142
69	T96570 Aname MYG067 NHF	0.186	0.192	0.181	0.181	0.178	0.151	0.189	0.159	0.156
70	T98759 Aname MYG185 NHK	0.197	0.197	0.195	0.189	0.192	0.178	0.208	0.173	0.162
71	T98900 Aname MYG034 NHJ	0.184	0.186	0.181	0.181	0.181	0.167	0.167	0.093	0.107
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.173	0.178	0.170	0.178	0.175	0.173	0.145	0.156	0.173
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.145	0.148	0.153	0.145	0.148	0.142	0.145	0.175	0.175
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.192	0.197	0.184	0.186	0.186	0.164	0.175	0.164	0.167
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.123	0.126	0.134	0.126	0.129	0.140	0.151	0.170	0.167
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.167	0.173	0.178	0.173	0.173	0.162	0.167	0.110	0.115
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.175	0.181	0.186	0.181	0.181	0.173	0.170	0.112	0.123
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.129	0.129	0.134	0.126	0.129	0.145	0.151	0.173	0.167
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.132	0.134	0.142	0.134	0.137	0.142	0.151	0.164	0.170
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.132	0.134	0.140	0.132	0.134	0.145	0.151	0.173	0.173
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.126	0.129	0.137	0.129	0.132	0.142	0.151	0.173	0.173
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.126	0.129	0.134	0.126	0.129	0.142	0.148	0.170	0.170
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.126	0.129	0.137	0.129	0.132	0.145	0.153	0.175	0.175
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.129	0.132	0.140	0.132	0.134	0.140	0.156	0.170	0.167

		1	2	3	4	5	6	7	8	9
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.129	0.132	0.137	0.129	0.132	0.142	0.148	0.170	0.170
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.164	0.170	0.164	0.162	0.162	0.148	0.175	0.118	0.140
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.164	0.170	0.164	0.162	0.162	0.148	0.175	0.118	0.140
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.167	0.173	0.167	0.164	0.164	0.151	0.173	0.115	0.142
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.167	0.173	0.167	0.164	0.164	0.151	0.178	0.121	0.142
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.164	0.170	0.170	0.167	0.167	0.153	0.170	0.118	0.134
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.167	0.173	0.167	0.164	0.164	0.153	0.173	0.118	0.134
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.129	0.132	0.137	0.129	0.132	0.142	0.156	0.178	0.173
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.134	0.137	0.132	0.132	0.129	0.181	0.153	0.173	0.170
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.134	0.137	0.132	0.132	0.129	0.181	0.153	0.173	0.170
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.121	0.126	0.129	0.134	0.132	0.167	0.151	0.173	0.178
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.134	0.137	0.142	0.134	0.137	0.142	0.151	0.170	0.164
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.112	0.118	0.129	0.121	0.123	0.142	0.156	0.173	0.164
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.129	0.132	0.134	0.132	0.134	0.142	0.156	0.175	0.175
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.129	0.129	0.137	0.129	0.132	0.145	0.167	0.189	0.167
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.140	0.142	0.140	0.142	0.140	0.178	0.142	0.197	0.178
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.132	0.134	0.140	0.132	0.134	0.148	0.148	0.175	0.170
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.132	0.134	0.140	0.132	0.134	0.148	0.148	0.175	0.170
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.129	0.132	0.134	0.126	0.129	0.145	0.145	0.173	0.164
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.134	0.137	0.142	0.134	0.137	0.151	0.151	0.178	0.173
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.129	0.132	0.137	0.129	0.132	0.142	0.151	0.170	0.170
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.134	0.137	0.145	0.137	0.140	0.140	0.153	0.167	0.167
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.134	0.137	0.142	0.134	0.137	0.151	0.151	0.178	0.173
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.140	0.142	0.148	0.140	0.142	0.142	0.156	0.173	0.167
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.129	0.129	0.137	0.129	0.132	0.140	0.148	0.164	0.167
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.118	0.118	0.118	0.118	0.115	0.175	0.159	0.186	0.159
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110

		1	2	3	4	5	6	7	8	9
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.121	0.118	0.110	0.118	0.115	0.186	0.142	0.192	0.192
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.195	0.189	0.184	0.184	0.184	0.162	0.170	0.085	0.112
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.181	0.181	0.175	0.175	0.175	0.151	0.167	0.088	0.110
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.192	0.195	0.186	0.192	0.192	0.170	0.170	0.099	0.110
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.184	0.186	0.181	0.181	0.181	0.167	0.167	0.093	0.107

		10	11	12	13	14	15	16	17	18
1	PC12	0.021	0.018	0.018	0.018	0.019	0.020	0.020	0.020	0.020
2	PC27	0.021	0.018	0.018	0.018	0.019	0.020	0.020	0.020	0.020
3	PC29	0.021	0.018	0.018	0.018	0.019	0.020	0.020	0.020	0.020
4	PC13	0.021	0.018	0.018	0.018	0.019	0.019	0.020	0.020	0.020
5	PC28	0.021	0.018	0.018	0.018	0.019	0.020	0.020	0.020	0.020
6	PC18	0.019	0.020	0.019	0.020	0.021	0.020	0.020	0.019	0.020
7	PC15	0.020	0.018	0.019	0.020	0.020	0.018	0.020	0.020	0.019
8	PC16	0.019	0.020	0.020	0.021	0.021	0.020	0.017	0.015	0.019
9	PC26	0.020	0.021	0.020	0.021	0.021	0.019	0.018	0.016	0.018
10	NA_N1_AG1		0.020	0.021	0.021	0.021	0.020	0.019	0.019	0.020
11	NAA_N45_AS38	0.178		0.018	0.019	0.020	0.020	0.020	0.020	0.020
12	NAB_N46_AS41	0.192	0.129		0.018	0.019	0.020	0.020	0.020	0.019
13	NAD_N93_AC10	0.205	0.164	0.140		0.021	0.021	0.021	0.021	0.020
14	NAM_N49_AD14	0.211	0.175	0.153	0.197		0.021	0.020	0.021	0.021
15	NAO_N22_AD328	0.170	0.167	0.186	0.200	0.192		0.020	0.019	0.016
16	NAQ_N5_AD352	0.151	0.184	0.178	0.205	0.189	0.181		0.017	0.020
17	NAW_N6_AD429	0.148	0.178	0.167	0.203	0.197	0.162	0.123		0.020
18	NAX_N24_AD452	0.184	0.167	0.164	0.189	0.192	0.101	0.167	0.170	
19	NAZ_N6_AD457	0.151	0.186	0.175	0.203	0.189	0.164	0.121	0.082	0.164
20	NB_N16_AH8	0.192	0.175	0.195	0.203	0.197	0.142	0.167	0.186	0.145
21	NBC_N6_AD577	0.170	0.175	0.175	0.211	0.186	0.162	0.115	0.063	0.167
22	NBE_N46_AD583	0.195	0.156	0.110	0.153	0.175	0.173	0.186	0.195	0.159
23	NBM_N4_AD678	0.197	0.184	0.195	0.214	0.211	0.197	0.151	0.164	0.214
24	NBR_N14_AD746	0.175	0.186	0.184	0.205	0.200	0.197	0.151	0.173	0.173
25	NBT_N7_AD748	0.162	0.189	0.197	0.216	0.195	0.170	0.118	0.107	0.189
26	NBU_N15_AD753	0.184	0.162	0.164	0.208	0.200	0.186	0.159	0.170	0.156
27	NBW_N50_AD784	0.189	0.186	0.173	0.197	0.159	0.186	0.184	0.181	0.200
28	NCA_N20_AF78	0.195	0.184	0.181	0.208	0.203	0.096	0.173	0.189	0.096

		10	11	12	13	14	15	16	17	18
29	NCG_N95_I16	0.197	0.137	0.156	0.134	0.178	0.186	0.178	0.186	0.184
30	NCU_N110_O211	0.162	0.175	0.208	0.203	0.216	0.167	0.156	0.164	0.173
31	NCW_N66_O280	0.162	0.184	0.195	0.192	0.189	0.178	0.148	0.142	0.159
32	NCY_N67_O282	0.195	0.214	0.219	0.230	0.219	0.170	0.175	0.137	0.181
33	NCZ_N110_O285	0.162	0.189	0.197	0.186	0.205	0.186	0.137	0.145	0.178
34	NDD_N101_O292	0.192	0.181	0.184	0.197	0.208	0.181	0.159	0.151	0.175
35	NDK_N94_O333	0.211	0.153	0.142	0.164	0.173	0.162	0.175	0.178	0.173
36	NDL_N96_O334	0.189	0.112	0.145	0.159	0.173	0.181	0.175	0.178	0.192
37	NEH_N112_BI22	0.170	0.181	0.195	0.219	0.192	0.186	0.126	0.126	0.203
38	NEM_N43_DW15	0.211	0.197	0.181	0.167	0.186	0.197	0.178	0.189	0.192
39	NEM_N43_AT53	0.214	0.195	0.178	0.170	0.189	0.200	0.181	0.186	0.195
40	NEW_N19_AD381	0.216	0.184	0.197	0.219	0.197	0.101	0.186	0.178	0.085
41	NFN_N43_CG5	0.227	0.181	0.170	0.151	0.181	0.203	0.181	0.200	0.192
42	NFO_N127_CB26	0.189	0.159	0.107	0.145	0.156	0.170	0.184	0.178	0.170
43	NFZ_N122_BV095	0.219	0.162	0.137	0.153	0.112	0.197	0.200	0.189	0.184
44	NGC_N129_CW5	0.197	0.156	0.148	0.153	0.186	0.192	0.162	0.164	0.192
45	NGE_N130_CW14	0.184	0.145	0.129	0.134	0.167	0.156	0.162	0.159	0.167
46	NGN_N19_DC5	0.197	0.181	0.186	0.197	0.197	0.085	0.162	0.173	0.077
47	NGS_N136_DG10	0.156	0.203	0.184	0.219	0.200	0.200	0.151	0.159	0.200
48	NGV_N35_DW21	0.186	0.159	0.162	0.151	0.167	0.189	0.164	0.162	0.186
49	NIG_N22+N23_ID10	0.178	0.175	0.192	0.211	0.184	0.074	0.173	0.186	0.090
50	NK_N36_AD110	0.192	0.153	0.148	0.145	0.164	0.205	0.167	0.159	0.200
51	NRF_N7_NN11	0.167	0.195	0.189	0.214	0.186	0.167	0.110	0.110	0.197
52	NRG_N7_NN15	0.159	0.192	0.189	0.214	0.186	0.164	0.112	0.101	0.195
53	NRH_N7_NN16	0.175	0.197	0.186	0.214	0.184	0.173	0.126	0.104	0.203
54	NRI_N7_NN17	0.167	0.195	0.192	0.216	0.192	0.170	0.118	0.104	0.200
55	NRJ_N7_NN18	0.173	0.195	0.195	0.216	0.189	0.170	0.123	0.101	0.200
56	NRK_N7_NN20	0.159	0.195	0.189	0.219	0.192	0.173	0.118	0.096	0.192

		10	11	12	13	14	15	16	17	18
57	NRL_N7_NN21	0.159	0.189	0.184	0.214	0.192	0.173	0.118	0.096	0.197
58	NRM_N7_NN37	0.173	0.208	0.208	0.227	0.208	0.189	0.126	0.118	0.214
59	NRO_N7_NN38	0.159	0.189	0.184	0.216	0.195	0.173	0.118	0.096	0.192
60	NRP_N138_NN35	0.167	0.192	0.175	0.192	0.205	0.159	0.132	0.112	0.164
61	NRQ_N138_NN36	0.173	0.195	0.173	0.195	0.205	0.164	0.140	0.115	0.170
62	NRW_N144_OU21	0.197	0.134	0.132	0.151	0.167	0.189	0.167	0.186	0.175
63	NY_N37_AR64	0.189	0.148	0.162	0.148	0.153	0.192	0.170	0.175	0.186
64	T101209 Kwonkan MYG175 NHP	0.197	0.134	0.126	0.145	0.164	0.189	0.170	0.181	0.175
65	T112084 Synothele MYG127 NHD	0.173	0.192	0.186	0.208	0.186	0.173	0.148	0.153	0.184
66	T112949 Aname MYG227 NHG	0.189	0.205	0.189	0.205	0.216	0.184	0.129	0.156	0.173
67	T121597 Aname MYG250 NHQ	0.189	0.123	0.132	0.140	0.156	0.162	0.164	0.173	0.164
68	T122062 Aname MYG182 NGX	0.184	0.189	0.192	0.203	0.200	0.186	0.159	0.162	0.178
69	T96570 Aname MYG067 NHF	0.178	0.197	0.189	0.225	0.211	0.181	0.145	0.159	0.164
70	T98759 Aname MYG185 NHK	0.170	0.216	0.225	0.249	0.211	0.205	0.140	0.153	0.200
71	T98900 Aname MYG034 NHJ	0.159	0.184	0.162	0.208	0.186	0.175	0.126	0.055	0.178
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.162	0.164	0.184	0.197	0.197	0.170	0.140	0.175	0.164
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.186	0.162	0.164	0.203	0.192	0.107	0.178	0.175	0.140
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.197	0.184	0.195	0.214	0.211	0.197	0.151	0.164	0.214
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.184	0.156	0.162	0.181	0.175	0.118	0.148	0.175	0.121
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.162	0.189	0.197	0.216	0.195	0.170	0.118	0.107	0.189
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.167	0.200	0.208	0.216	0.200	0.181	0.118	0.118	0.197
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.186	0.159	0.170	0.186	0.178	0.115	0.153	0.181	0.121
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.178	0.156	0.159	0.175	0.175	0.121	0.148	0.170	0.118
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.184	0.156	0.167	0.186	0.175	0.121	0.153	0.178	0.123
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.184	0.156	0.164	0.181	0.173	0.118	0.153	0.178	0.121
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.181	0.153	0.164	0.181	0.173	0.115	0.151	0.175	0.121
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.184	0.153	0.170	0.178	0.178	0.126	0.153	0.175	0.126
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.184	0.162	0.162	0.184	0.178	0.121	0.151	0.175	0.118

		10	11	12	13	14	15	16	17	18
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.181	0.153	0.164	0.184	0.175	0.118	0.151	0.175	0.121
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.167	0.178	0.192	0.216	0.189	0.184	0.123	0.123	0.200
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.167	0.178	0.192	0.216	0.189	0.184	0.123	0.123	0.200
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.164	0.181	0.195	0.219	0.186	0.181	0.121	0.121	0.197
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.170	0.181	0.195	0.219	0.192	0.186	0.126	0.126	0.203
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.162	0.175	0.186	0.203	0.200	0.178	0.121	0.121	0.192
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.164	0.178	0.184	0.205	0.197	0.181	0.118	0.118	0.195
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.184	0.153	0.167	0.184	0.173	0.118	0.159	0.175	0.123
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.203	0.173	0.156	0.153	0.162	0.175	0.162	0.181	0.162
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.203	0.173	0.156	0.153	0.162	0.175	0.162	0.181	0.162
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.189	0.123	0.132	0.140	0.156	0.162	0.164	0.173	0.164
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.181	0.164	0.173	0.184	0.175	0.123	0.151	0.178	0.118
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.170	0.151	0.159	0.170	0.178	0.110	0.151	0.170	0.115
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.184	0.156	0.153	0.181	0.175	0.129	0.148	0.178	0.132
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.192	0.170	0.181	0.192	0.186	0.129	0.164	0.189	0.121
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.189	0.159	0.107	0.145	0.156	0.170	0.184	0.178	0.170
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.186	0.159	0.170	0.186	0.175	0.115	0.156	0.181	0.121
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.186	0.159	0.170	0.186	0.175	0.115	0.156	0.181	0.121
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.184	0.156	0.167	0.189	0.175	0.112	0.151	0.178	0.121
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.189	0.162	0.170	0.184	0.178	0.118	0.159	0.184	0.123
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.181	0.159	0.164	0.178	0.175	0.123	0.151	0.175	0.121
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.181	0.164	0.167	0.184	0.175	0.118	0.151	0.173	0.115
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.189	0.162	0.170	0.184	0.178	0.118	0.159	0.184	0.123
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.178	0.167	0.167	0.178	0.175	0.123	0.142	0.167	0.123
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.178	0.159	0.170	0.181	0.175	0.115	0.148	0.170	0.118
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.211	0.153	0.142	0.164	0.173	0.162	0.175	0.178	0.173
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.148	0.178	0.167	0.203	0.197	0.162	0.123	0.000	0.170
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.148	0.178	0.167	0.203	0.197	0.162	0.123	0.000	0.170

		10	11	12	13	14	15	16	17	18
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.148	0.178	0.167	0.203	0.197	0.162	0.123	0.000	0.170
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.189	0.112	0.145	0.159	0.173	0.181	0.175	0.178	0.192
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.148	0.178	0.167	0.203	0.197	0.162	0.123	0.000	0.170
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.162	0.181	0.170	0.214	0.200	0.175	0.132	0.030	0.170
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.148	0.178	0.167	0.203	0.197	0.162	0.123	0.000	0.170
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.170	0.175	0.175	0.211	0.186	0.162	0.115	0.063	0.167
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.159	0.184	0.162	0.208	0.186	0.175	0.126	0.055	0.178

		19	20	21	22	23	24	25	26	27
1	PC12	0.019	0.019	0.021	0.018	0.021	0.020	0.020	0.020	0.020
2	PC27	0.019	0.019	0.021	0.018	0.021	0.020	0.020	0.019	0.019
3	PC29	0.019	0.019	0.020	0.018	0.020	0.020	0.020	0.019	0.019
4	PC13	0.019	0.019	0.021	0.018	0.020	0.020	0.020	0.019	0.019
5	PC28	0.019	0.019	0.021	0.018	0.020	0.020	0.020	0.019	0.019
6	PC18	0.018	0.019	0.020	0.020	0.019	0.020	0.019	0.019	0.020
7	PC15	0.019	0.019	0.020	0.019	0.020	0.020	0.020	0.021	0.020
8	PC16	0.015	0.020	0.016	0.021	0.019	0.020	0.016	0.020	0.020
9	PC26	0.016	0.021	0.016	0.020	0.020	0.020	0.017	0.019	0.020
10	NA_N1_AG1	0.019	0.021	0.020	0.021	0.021	0.020	0.019	0.020	0.020
11	NAA_N45_AS38	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.019	0.020
12	NAB_N46_AS41	0.020	0.021	0.020	0.016	0.021	0.020	0.021	0.019	0.020
13	NAD_N93_AC10	0.021	0.021	0.021	0.019	0.021	0.021	0.022	0.021	0.021
14	NAM_N49_AD14	0.020	0.021	0.020	0.020	0.021	0.021	0.021	0.021	0.019
15	NAO_N22_AD328	0.019	0.018	0.019	0.020	0.021	0.021	0.020	0.020	0.020
16	NAQ_N5_AD352	0.017	0.020	0.017	0.020	0.019	0.019	0.017	0.019	0.020
17	NAW_N6_AD429	0.014	0.020	0.013	0.021	0.019	0.020	0.016	0.020	0.020
18	NAX_N24_AD452	0.019	0.018	0.020	0.019	0.021	0.020	0.020	0.019	0.021
19	NAZ_N6_AD457		0.020	0.014	0.021	0.019	0.020	0.017	0.018	0.020
20	NB_N16_AH8	0.173		0.020	0.021	0.021	0.021	0.020	0.020	0.022
21	NBC_N6_AD577	0.077	0.189		0.021	0.019	0.020	0.017	0.019	0.020
22	NBE_N46_AD583	0.200	0.192	0.192		0.021	0.020	0.021	0.019	0.021
23	NBM_N4_AD678	0.162	0.214	0.156	0.208		0.021	0.018	0.020	0.020
24	NBR_N14_AD746	0.175	0.195	0.178	0.184	0.197		0.019	0.017	0.020
25	NBT_N7_AD748	0.112	0.181	0.123	0.205	0.134	0.164		0.019	0.020
26	NBU_N15_AD753	0.142	0.173	0.156	0.159	0.186	0.112	0.164		0.019
27	NBW_N50_AD784	0.178	0.216	0.178	0.192	0.175	0.175	0.181	0.162	
28	NCA_N20_AF78	0.184	0.167	0.178	0.186	0.208	0.189	0.205	0.189	0.203

		19	20	21	22	23	24	25	26	27
29	NCG_N95_I16	0.197	0.184	0.184	0.148	0.186	0.178	0.192	0.200	0.200
30	NCU_N110_O211	0.145	0.159	0.164	0.184	0.164	0.184	0.167	0.167	0.181
31	NCW_N66_O280	0.151	0.159	0.153	0.200	0.142	0.159	0.126	0.162	0.184
32	NCY_N67_O282	0.167	0.203	0.153	0.211	0.175	0.197	0.156	0.178	0.216
33	NCZ_N110_O285	0.137	0.170	0.153	0.181	0.162	0.178	0.162	0.151	0.195
34	NDD_N101_O292	0.159	0.159	0.156	0.189	0.186	0.192	0.178	0.181	0.173
35	NDK_N94_O333	0.173	0.189	0.195	0.159	0.195	0.203	0.189	0.189	0.184
36	NDL_N96_O334	0.189	0.192	0.181	0.162	0.178	0.208	0.200	0.203	0.178
37	NEH_N112_BI22	0.123	0.178	0.126	0.192	0.142	0.178	0.101	0.164	0.178
38	NEM_N43_DW15	0.186	0.164	0.203	0.186	0.200	0.189	0.203	0.205	0.197
39	NEM_N43_AT53	0.189	0.162	0.200	0.184	0.203	0.186	0.197	0.203	0.200
40	NEW_N19_AD381	0.175	0.164	0.156	0.186	0.208	0.192	0.192	0.178	0.219
41	NFN_N43_CG5	0.200	0.167	0.208	0.189	0.203	0.186	0.208	0.203	0.192
42	NFO_N127_CB26	0.192	0.184	0.178	0.104	0.195	0.192	0.203	0.175	0.178
43	NFZ_N122_BV095	0.186	0.203	0.189	0.162	0.178	0.197	0.197	0.181	0.148
44	NGC_N129_CW5	0.186	0.186	0.178	0.153	0.186	0.189	0.197	0.170	0.175
45	NGE_N130_CW14	0.170	0.170	0.159	0.148	0.205	0.192	0.195	0.170	0.192
46	NGN_N19_DC5	0.178	0.140	0.164	0.192	0.205	0.173	0.192	0.184	0.195
47	NGS_N136_DG10	0.145	0.192	0.156	0.184	0.148	0.178	0.134	0.181	0.203
48	NGV_N35_DW21	0.170	0.178	0.173	0.167	0.189	0.178	0.189	0.164	0.173
49	NIG_N22+N23_ID10	0.186	0.148	0.167	0.184	0.208	0.192	0.197	0.192	0.200
50	NK_N36_AD110	0.162	0.208	0.173	0.173	0.192	0.164	0.205	0.186	0.181
51	NRF_N7_NN11	0.115	0.192	0.118	0.214	0.137	0.181	0.047	0.173	0.156
52	NRG_N7_NN15	0.118	0.189	0.121	0.214	0.137	0.178	0.038	0.175	0.159
53	NRH_N7_NN16	0.129	0.189	0.129	0.216	0.145	0.192	0.049	0.189	0.175
54	NRI_N7_NN17	0.126	0.186	0.129	0.219	0.145	0.186	0.047	0.184	0.167
55	NRJ_N7_NN18	0.126	0.186	0.126	0.219	0.142	0.189	0.047	0.186	0.170
56	NRK_N7_NN20	0.126	0.197	0.115	0.216	0.140	0.170	0.047	0.175	0.167

		19	20	21	22	23	24	25	26	27
57	NRL_N7_NN21	0.126	0.197	0.115	0.211	0.134	0.170	0.047	0.170	0.167
58	NRM_N7_NN37	0.142	0.181	0.140	0.230	0.148	0.186	0.063	0.195	0.189
59	NRO_N7_NN38	0.126	0.197	0.115	0.216	0.137	0.167	0.047	0.170	0.162
60	NRP_N138_NN35	0.126	0.184	0.121	0.170	0.167	0.186	0.137	0.175	0.192
61	NRQ_N138_NN36	0.132	0.186	0.126	0.173	0.173	0.189	0.137	0.178	0.197
62	NRW_N144_OU21	0.167	0.197	0.175	0.153	0.186	0.195	0.195	0.164	0.186
63	NY_N37_AR64	0.178	0.181	0.189	0.159	0.197	0.178	0.192	0.175	0.186
64	T101209 Kwonkan MYG175 NHP	0.167	0.192	0.173	0.151	0.189	0.195	0.195	0.170	0.186
65	T112084 Synothele MYG127 NHD	0.153	0.162	0.151	0.195	0.162	0.178	0.156	0.178	0.192
66	T112949 Aname MYG227 NHG	0.156	0.178	0.156	0.170	0.178	0.178	0.151	0.178	0.184
67	T121597 Aname MYG250 NHQ	0.173	0.181	0.170	0.153	0.184	0.189	0.186	0.156	0.167
68	T122062 Aname MYG182 NGX	0.170	0.203	0.178	0.186	0.153	0.186	0.159	0.178	0.195
69	T96570 Aname MYG067 NHF	0.156	0.192	0.159	0.205	0.153	0.178	0.164	0.175	0.192
70	T98759 Aname MYG185 NHK	0.145	0.178	0.151	0.203	0.184	0.189	0.170	0.178	0.205
71	T98900 Aname MYG034 NHJ	0.093	0.184	0.079	0.192	0.156	0.173	0.126	0.173	0.184
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.167	0.164	0.162	0.164	0.189	0.173	0.175	0.178	0.200
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.162	0.079	0.178	0.178	0.208	0.181	0.178	0.167	0.200
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.162	0.214	0.156	0.208	0.000	0.197	0.134	0.186	0.175
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.148	0.079	0.162	0.151	0.189	0.178	0.164	0.145	0.181
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.112	0.181	0.123	0.205	0.134	0.164	0.000	0.164	0.181
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.129	0.186	0.137	0.216	0.137	0.167	0.019	0.181	0.178
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.153	0.077	0.170	0.153	0.189	0.178	0.167	0.148	0.178
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.153	0.077	0.159	0.159	0.189	0.175	0.164	0.145	0.178
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.153	0.079	0.167	0.159	0.186	0.184	0.164	0.151	0.178
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.153	0.077	0.167	0.153	0.186	0.184	0.164	0.148	0.178
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.151	0.074	0.164	0.153	0.186	0.181	0.164	0.148	0.178
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.148	0.077	0.162	0.159	0.195	0.181	0.167	0.151	0.184
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.151	0.079	0.162	0.156	0.186	0.181	0.162	0.142	0.181

		19	20	21	22	23	24	25	26	27
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.151	0.077	0.164	0.156	0.186	0.181	0.164	0.148	0.178
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.121	0.175	0.123	0.195	0.140	0.175	0.099	0.167	0.175
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.121	0.175	0.123	0.195	0.140	0.175	0.099	0.167	0.175
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.118	0.173	0.121	0.197	0.142	0.178	0.096	0.170	0.178
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.123	0.178	0.126	0.192	0.142	0.178	0.101	0.164	0.178
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.118	0.181	0.115	0.192	0.132	0.173	0.090	0.159	0.175
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.121	0.184	0.118	0.189	0.129	0.175	0.090	0.162	0.178
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.151	0.079	0.164	0.156	0.192	0.184	0.164	0.151	0.181
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.184	0.175	0.181	0.167	0.197	0.192	0.197	0.211	0.192
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.184	0.175	0.181	0.167	0.197	0.192	0.197	0.211	0.192
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.173	0.181	0.170	0.153	0.184	0.189	0.186	0.156	0.167
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.153	0.066	0.167	0.159	0.192	0.175	0.167	0.153	0.186
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.151	0.082	0.170	0.151	0.189	0.186	0.167	0.151	0.175
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.156	0.088	0.167	0.153	0.184	0.184	0.173	0.148	0.173
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.156	0.088	0.178	0.164	0.211	0.167	0.184	0.145	0.186
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.192	0.184	0.178	0.104	0.195	0.192	0.203	0.175	0.178
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.156	0.074	0.170	0.159	0.189	0.181	0.167	0.153	0.181
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.156	0.074	0.170	0.159	0.189	0.181	0.167	0.153	0.181
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.151	0.074	0.164	0.156	0.186	0.178	0.164	0.151	0.178
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.159	0.077	0.173	0.162	0.192	0.184	0.170	0.156	0.184
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.151	0.077	0.164	0.159	0.181	0.175	0.164	0.148	0.184
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.151	0.079	0.162	0.162	0.184	0.184	0.164	0.148	0.178
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.159	0.077	0.173	0.162	0.192	0.184	0.170	0.156	0.184
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.148	0.082	0.156	0.162	0.175	0.189	0.167	0.156	0.186
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.145	0.079	0.162	0.151	0.181	0.184	0.167	0.148	0.175
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.173	0.189	0.195	0.159	0.195	0.203	0.189	0.189	0.184
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.082	0.186	0.063	0.195	0.164	0.173	0.107	0.170	0.181
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.082	0.186	0.063	0.195	0.164	0.173	0.107	0.170	0.181

		19	20	21	22	23	24	25	26	27
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.082	0.186	0.063	0.195	0.164	0.173	0.107	0.170	0.181
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.189	0.192	0.181	0.162	0.178	0.208	0.200	0.203	0.178
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.082	0.186	0.063	0.195	0.164	0.173	0.107	0.170	0.181
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.093	0.195	0.077	0.195	0.162	0.175	0.129	0.173	0.178
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.082	0.186	0.063	0.195	0.164	0.173	0.107	0.170	0.181
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.077	0.189	0.000	0.192	0.156	0.178	0.123	0.156	0.178
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.093	0.184	0.079	0.192	0.156	0.173	0.126	0.173	0.184

		28	29	30	31	32	33	34	35	36
1	PC12	0.020	0.017	0.019	0.020	0.021	0.019	0.020	0.017	0.017
2	PC27	0.021	0.017	0.019	0.020	0.021	0.020	0.020	0.017	0.017
3	PC29	0.020	0.017	0.019	0.020	0.021	0.020	0.020	0.017	0.016
4	PC13	0.020	0.017	0.019	0.020	0.021	0.019	0.020	0.017	0.017
5	PC28	0.020	0.017	0.019	0.020	0.021	0.019	0.020	0.017	0.017
6	PC18	0.020	0.020	0.018	0.019	0.019	0.019	0.019	0.020	0.020
7	PC15	0.019	0.019	0.020	0.019	0.020	0.019	0.020	0.019	0.018
8	PC16	0.020	0.020	0.020	0.018	0.019	0.020	0.019	0.020	0.021
9	PC26	0.020	0.020	0.019	0.018	0.019	0.018	0.020	0.019	0.021
10	NA_N1_AG1	0.021	0.021	0.019	0.019	0.021	0.019	0.021	0.021	0.020
11	NAA_N45_AS38	0.020	0.018	0.020	0.020	0.021	0.020	0.020	0.019	0.017
12	NAB_N46_AS41	0.020	0.019	0.021	0.021	0.022	0.021	0.020	0.018	0.018
13	NAD_N93_AC10	0.021	0.018	0.021	0.021	0.022	0.020	0.021	0.019	0.019
14	NAM_N49_AD14	0.021	0.020	0.022	0.020	0.022	0.021	0.021	0.020	0.020
15	NAO_N22_AD328	0.015	0.020	0.020	0.020	0.020	0.020	0.020	0.019	0.020
16	NAQ_N5_AD352	0.020	0.020	0.019	0.019	0.020	0.018	0.019	0.020	0.020
17	NAW_N6_AD429	0.020	0.020	0.019	0.018	0.018	0.018	0.019	0.020	0.020
18	NAX_N24_AD452	0.015	0.020	0.020	0.019	0.020	0.020	0.020	0.020	0.021
19	NAZ_N6_AD457	0.020	0.021	0.018	0.019	0.020	0.018	0.019	0.020	0.020
20	NB_N16_AH8	0.020	0.020	0.019	0.019	0.021	0.020	0.019	0.020	0.021
21	NBC_N6_AD577	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.021	0.020
22	NBE_N46_AD583	0.020	0.019	0.020	0.021	0.021	0.020	0.020	0.019	0.019
23	NBM_N4_AD678	0.021	0.020	0.019	0.018	0.020	0.019	0.020	0.021	0.020
24	NBR_N14_AD746	0.020	0.020	0.020	0.019	0.021	0.020	0.021	0.021	0.021
25	NBT_N7_AD748	0.021	0.021	0.020	0.017	0.019	0.019	0.020	0.020	0.021
26	NBU_N15_AD753	0.020	0.021	0.020	0.019	0.020	0.019	0.020	0.020	0.021
27	NBW_N50_AD784	0.021	0.021	0.020	0.020	0.022	0.021	0.020	0.020	0.020
28	NCA_N20_AF78		0.020	0.020	0.021	0.020	0.021	0.020	0.020	0.020

		28	29	30	31	32	33	34	35	36
29	NCG_N95_I16	0.189		0.020	0.020	0.021	0.020	0.020	0.018	0.016
30	NCU_N110_O211	0.189	0.184		0.016	0.018	0.013	0.019	0.020	0.020
31	NCW_N66_O280	0.200	0.173	0.104		0.018	0.016	0.019	0.020	0.020
32	NCY_N67_O282	0.189	0.208	0.137	0.137		0.018	0.019	0.021	0.022
33	NCZ_N110_O285	0.195	0.184	0.068	0.110	0.134		0.019	0.019	0.021
34	NDD_N101_O292	0.175	0.184	0.156	0.159	0.164	0.162		0.021	0.021
35	NDK_N94_O333	0.184	0.134	0.186	0.181	0.205	0.153	0.197		0.018
36	NDL_N96_O334	0.189	0.104	0.181	0.186	0.222	0.195	0.197	0.145	
37	NEH_N112_BI22	0.216	0.195	0.153	0.137	0.148	0.142	0.142	0.175	0.189
38	NEM_N43_DW15	0.197	0.162	0.200	0.192	0.211	0.181	0.178	0.170	0.178
39	NEM_N43_AT53	0.200	0.164	0.203	0.195	0.208	0.184	0.181	0.173	0.181
40	NEW_N19_AD381	0.110	0.197	0.195	0.173	0.173	0.192	0.192	0.181	0.205
41	NFN_N43_CG5	0.192	0.162	0.197	0.189	0.216	0.200	0.175	0.186	0.178
42	NFO_N127_CB26	0.195	0.156	0.197	0.197	0.195	0.170	0.186	0.148	0.153
43	NFZ_N122_BV095	0.197	0.175	0.189	0.175	0.216	0.167	0.197	0.162	0.170
44	NGC_N129_CW5	0.203	0.148	0.178	0.175	0.197	0.170	0.167	0.151	0.145
45	NGE_N130_CW14	0.164	0.132	0.181	0.181	0.197	0.167	0.184	0.140	0.126
46	NGN_N19_DC5	0.052	0.192	0.181	0.181	0.173	0.181	0.173	0.175	0.192
47	NGS_N136_DG10	0.222	0.203	0.186	0.164	0.175	0.184	0.170	0.214	0.214
48	NGV_N35_DW21	0.197	0.156	0.189	0.173	0.208	0.178	0.159	0.164	0.162
49	NIG_N22+N23_ID10	0.085	0.186	0.184	0.175	0.184	0.184	0.181	0.170	0.189
50	NK_N36_AD110	0.211	0.162	0.186	0.175	0.200	0.167	0.162	0.162	0.156
51	NRF_N7_NN11	0.195	0.192	0.156	0.123	0.153	0.156	0.184	0.173	0.189
52	NRG_N7_NN15	0.192	0.192	0.153	0.121	0.148	0.148	0.186	0.170	0.189
53	NRH_N7_NN16	0.205	0.197	0.164	0.123	0.162	0.151	0.192	0.175	0.184
54	NRI_N7_NN17	0.195	0.197	0.162	0.123	0.162	0.156	0.189	0.175	0.184
55	NRJ_N7_NN18	0.197	0.195	0.162	0.121	0.159	0.153	0.189	0.175	0.181
56	NRK_N7_NN20	0.197	0.181	0.162	0.121	0.148	0.159	0.181	0.175	0.186

		28	29	30	31	32	33	34	35	36
57	NRL_N7_NN21	0.203	0.181	0.162	0.115	0.148	0.153	0.181	0.170	0.181
58	NRM_N7_NN37	0.225	0.200	0.162	0.129	0.164	0.159	0.186	0.197	0.214
59	NRO_N7_NN38	0.203	0.178	0.156	0.115	0.142	0.153	0.175	0.173	0.184
60	NRP_N138_NN35	0.173	0.184	0.164	0.148	0.153	0.140	0.162	0.178	0.200
61	NRQ_N138_NN36	0.181	0.192	0.170	0.153	0.159	0.148	0.170	0.186	0.203
62	NRW_N144_OU21	0.178	0.156	0.192	0.192	0.227	0.181	0.184	0.137	0.134
63	NY_N37_AR64	0.197	0.167	0.173	0.170	0.203	0.156	0.173	0.181	0.156
64	T101209 Kwonkan MYG175 NHP	0.181	0.153	0.186	0.186	0.222	0.181	0.184	0.132	0.132
65	T112084 Synothele MYG127 NHD	0.195	0.184	0.162	0.132	0.173	0.167	0.164	0.203	0.200
66	T112949 Aname MYG227 NHG	0.170	0.173	0.153	0.140	0.181	0.153	0.148	0.189	0.197
67	T121597 Aname MYG250 NHQ	0.186	0.123	0.170	0.173	0.214	0.170	0.175	0.140	0.123
68	T122062 Aname MYG182 NGX	0.195	0.181	0.140	0.134	0.156	0.129	0.156	0.175	0.181
69	T96570 Aname MYG067 NHF	0.192	0.184	0.156	0.156	0.162	0.153	0.162	0.181	0.203
70	T98759 Aname MYG185 NHK	0.211	0.219	0.181	0.170	0.184	0.164	0.189	0.195	0.208
71	T98900 Aname MYG034 NHJ	0.184	0.181	0.167	0.142	0.162	0.156	0.170	0.189	0.170
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.184	0.181	0.170	0.159	0.184	0.173	0.181	0.208	0.189
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.142	0.173	0.156	0.175	0.175	0.173	0.156	0.178	0.175
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.208	0.186	0.164	0.142	0.175	0.162	0.186	0.195	0.178
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.153	0.164	0.145	0.148	0.173	0.153	0.140	0.170	0.170
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.205	0.192	0.167	0.126	0.156	0.162	0.178	0.189	0.200
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.211	0.195	0.164	0.129	0.159	0.164	0.181	0.197	0.203
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.156	0.170	0.142	0.142	0.170	0.156	0.145	0.173	0.175
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.151	0.153	0.153	0.140	0.170	0.151	0.134	0.173	0.170
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.153	0.167	0.151	0.148	0.170	0.153	0.142	0.175	0.173
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.153	0.164	0.148	0.145	0.170	0.151	0.140	0.170	0.170
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.151	0.162	0.145	0.148	0.167	0.148	0.140	0.173	0.167
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.159	0.170	0.145	0.148	0.175	0.148	0.140	0.170	0.173
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.156	0.159	0.151	0.142	0.178	0.159	0.142	0.173	0.175

		28	29	30	31	32	33	34	35	36
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.151	0.164	0.148	0.148	0.167	0.151	0.140	0.175	0.170
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.214	0.192	0.151	0.134	0.145	0.140	0.140	0.173	0.186
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.214	0.192	0.151	0.134	0.145	0.140	0.140	0.173	0.186
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.211	0.195	0.153	0.137	0.148	0.142	0.142	0.175	0.189
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.216	0.195	0.153	0.137	0.148	0.142	0.142	0.175	0.189
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.211	0.181	0.145	0.123	0.148	0.134	0.140	0.175	0.184
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.214	0.184	0.148	0.126	0.145	0.137	0.137	0.173	0.186
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.153	0.170	0.148	0.153	0.167	0.151	0.142	0.175	0.170
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.173	0.132	0.173	0.192	0.208	0.186	0.186	0.159	0.140
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.173	0.132	0.173	0.192	0.208	0.186	0.186	0.159	0.140
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.186	0.123	0.170	0.173	0.214	0.170	0.175	0.140	0.123
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.159	0.162	0.148	0.142	0.173	0.156	0.145	0.173	0.175
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.145	0.167	0.137	0.145	0.167	0.140	0.134	0.162	0.162
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.159	0.164	0.148	0.153	0.181	0.153	0.145	0.173	0.173
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.159	0.186	0.142	0.156	0.181	0.159	0.153	0.181	0.175
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.195	0.156	0.197	0.197	0.195	0.170	0.186	0.148	0.153
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.156	0.167	0.145	0.145	0.167	0.153	0.145	0.175	0.173
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.156	0.167	0.145	0.145	0.167	0.153	0.145	0.175	0.173
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.153	0.164	0.140	0.145	0.167	0.156	0.148	0.173	0.170
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.159	0.170	0.148	0.148	0.170	0.156	0.148	0.178	0.175
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.153	0.159	0.153	0.148	0.173	0.156	0.140	0.175	0.170
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.153	0.156	0.151	0.140	0.173	0.153	0.137	0.173	0.173
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.159	0.170	0.148	0.148	0.170	0.156	0.148	0.178	0.175
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.159	0.153	0.153	0.151	0.170	0.145	0.137	0.175	0.175
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.151	0.164	0.140	0.137	0.162	0.142	0.134	0.170	0.170
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.184	0.134	0.186	0.181	0.205	0.153	0.197	0.000	0.145
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.189	0.186	0.164	0.142	0.137	0.145	0.151	0.178	0.178
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.189	0.186	0.164	0.142	0.137	0.145	0.151	0.178	0.178

		28	29	30	31	32	33	34	35	36
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.189	0.186	0.164	0.142	0.137	0.145	0.151	0.178	0.178
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.189	0.104	0.181	0.186	0.222	0.195	0.197	0.145	0.000
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.189	0.186	0.164	0.142	0.137	0.145	0.151	0.178	0.178
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.192	0.186	0.164	0.148	0.153	0.151	0.153	0.186	0.178
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.189	0.186	0.164	0.142	0.137	0.145	0.151	0.178	0.178
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.178	0.184	0.164	0.153	0.153	0.153	0.156	0.195	0.181
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.184	0.181	0.167	0.142	0.162	0.156	0.170	0.189	0.170

		37	38	39	40	41	42	43	44	45
1	PC12	0.020	0.018	0.018	0.020	0.018	0.018	0.019	0.017	0.017
2	PC27	0.020	0.018	0.018	0.020	0.018	0.018	0.019	0.017	0.017
3	PC29	0.020	0.018	0.018	0.021	0.018	0.018	0.019	0.017	0.017
4	PC13	0.019	0.018	0.018	0.020	0.018	0.018	0.019	0.017	0.017
5	PC28	0.019	0.018	0.018	0.020	0.018	0.018	0.019	0.017	0.017
6	PC18	0.019	0.020	0.020	0.021	0.020	0.020	0.020	0.019	0.019
7	PC15	0.020	0.019	0.019	0.019	0.020	0.018	0.020	0.019	0.018
8	PC16	0.017	0.021	0.021	0.020	0.021	0.021	0.021	0.020	0.020
9	PC26	0.018	0.021	0.021	0.020	0.021	0.020	0.021	0.020	0.020
10	NA_N1_AG1	0.020	0.021	0.021	0.022	0.022	0.020	0.022	0.021	0.020
11	NAA_N45_AS38	0.020	0.021	0.021	0.020	0.020	0.019	0.019	0.019	0.018
12	NAB_N46_AS41	0.021	0.020	0.020	0.021	0.020	0.016	0.018	0.019	0.018
13	NAD_N93_AC10	0.022	0.020	0.020	0.022	0.019	0.018	0.019	0.019	0.018
14	NAM_N49_AD14	0.021	0.020	0.020	0.021	0.020	0.019	0.017	0.020	0.020
15	NAO_N22_AD328	0.020	0.021	0.021	0.016	0.021	0.020	0.021	0.021	0.019
16	NAQ_N5_AD352	0.017	0.020	0.020	0.020	0.020	0.020	0.021	0.019	0.019
17	NAW_N6_AD429	0.017	0.020	0.020	0.020	0.021	0.020	0.020	0.019	0.019
18	NAX_N24_AD452	0.021	0.021	0.021	0.015	0.021	0.020	0.020	0.021	0.020
19	NAZ_N6_AD457	0.017	0.020	0.020	0.020	0.021	0.021	0.020	0.020	0.020
20	NB_N16_AH8	0.020	0.019	0.019	0.019	0.020	0.020	0.021	0.020	0.020
21	NBC_N6_AD577	0.017	0.021	0.021	0.019	0.021	0.020	0.020	0.020	0.019
22	NBE_N46_AD583	0.021	0.020	0.020	0.020	0.020	0.016	0.019	0.019	0.019
23	NBM_N4_AD678	0.018	0.021	0.021	0.021	0.021	0.021	0.020	0.020	0.021
24	NBR_N14_AD746	0.020	0.020	0.020	0.021	0.020	0.021	0.021	0.020	0.021
25	NBT_N7_AD748	0.016	0.021	0.021	0.021	0.021	0.021	0.021	0.021	0.021
26	NBU_N15_AD753	0.019	0.021	0.021	0.020	0.021	0.020	0.020	0.020	0.020
27	NBW_N50_AD784	0.020	0.021	0.021	0.022	0.021	0.020	0.019	0.020	0.021
28	NCA_N20_AF78	0.022	0.021	0.021	0.016	0.021	0.021	0.021	0.021	0.019

		37	38	39	40	41	42	43	44	45
29	NCG_N95_I16	0.021	0.019	0.019	0.021	0.019	0.019	0.020	0.019	0.018
30	NCU_N110_O211	0.019	0.021	0.021	0.021	0.021	0.021	0.020	0.020	0.020
31	NCW_N66_O280	0.018	0.021	0.021	0.020	0.020	0.021	0.020	0.020	0.020
32	NCY_N67_O282	0.019	0.021	0.021	0.020	0.022	0.021	0.022	0.021	0.021
33	NCZ_N110_O285	0.018	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020
34	NDD_N101_O292	0.018	0.020	0.020	0.021	0.020	0.020	0.021	0.020	0.020
35	NDK_N94_O333	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.018
36	NDL_N96_O334	0.020	0.020	0.020	0.021	0.020	0.019	0.020	0.018	0.017
37	NEH_N112_BI22		0.021	0.021	0.021	0.021	0.020	0.021	0.020	0.021
38	NEM_N43_DW15	0.208		0.005	0.021	0.011	0.020	0.020	0.019	0.019
39	NEM_N43_AT53	0.203	0.008		0.021	0.011	0.019	0.020	0.019	0.020
40	NEW_N19_AD381	0.195	0.205	0.203		0.021	0.020	0.021	0.021	0.020
41	NFN_N43_CG5	0.214	0.049	0.047	0.211		0.020	0.020	0.019	0.019
42	NFO_N127_CB26	0.184	0.173	0.164	0.181	0.184		0.018	0.018	0.018
43	NFZ_N122_BV095	0.197	0.178	0.175	0.192	0.170	0.137		0.020	0.020
44	NGC_N129_CW5	0.181	0.159	0.162	0.208	0.162	0.145	0.170		0.018
45	NGE_N130_CW14	0.192	0.164	0.167	0.167	0.164	0.134	0.170	0.140	
46	NGN_N19_DC5	0.203	0.195	0.197	0.090	0.189	0.189	0.189	0.203	0.167
47	NGS_N136_DG10	0.132	0.208	0.203	0.214	0.208	0.186	0.205	0.205	0.195
48	NGV_N35_DW21	0.197	0.140	0.142	0.186	0.148	0.156	0.159	0.151	0.140
49	NIG_N22+N23_ID10	0.200	0.200	0.203	0.085	0.203	0.192	0.200	0.211	0.145
50	NK_N36_AD110	0.162	0.170	0.173	0.197	0.170	0.151	0.175	0.159	0.153
51	NRF_N7_NN11	0.085	0.208	0.208	0.178	0.214	0.195	0.197	0.189	0.192
52	NRG_N7_NN15	0.088	0.203	0.203	0.186	0.214	0.195	0.197	0.189	0.186
53	NRH_N7_NN16	0.096	0.214	0.214	0.195	0.222	0.197	0.203	0.203	0.184
54	NRI_N7_NN17	0.096	0.208	0.208	0.192	0.216	0.200	0.203	0.197	0.189
55	NRJ_N7_NN18	0.093	0.208	0.208	0.192	0.216	0.200	0.203	0.197	0.186
56	NRK_N7_NN20	0.090	0.208	0.205	0.186	0.214	0.195	0.205	0.189	0.184

		37	38	39	40	41	42	43	44	45
57	NRL_N7_NN21	0.085	0.203	0.200	0.186	0.214	0.189	0.200	0.184	0.184
58	NRM_N7_NN37	0.107	0.211	0.211	0.211	0.214	0.219	0.214	0.203	0.197
59	NRO_N7_NN38	0.085	0.205	0.203	0.186	0.211	0.195	0.205	0.186	0.186
60	NRP_N138_NN35	0.129	0.200	0.203	0.167	0.197	0.164	0.175	0.170	0.170
61	NRQ_N138_NN36	0.129	0.208	0.205	0.173	0.200	0.167	0.175	0.178	0.178
62	NRW_N144_OU21	0.186	0.170	0.173	0.178	0.170	0.145	0.140	0.142	0.132
63	NY_N37_AR64	0.175	0.170	0.167	0.197	0.170	0.151	0.156	0.173	0.145
64	T101209 Kwonkan MYG175 NHP	0.181	0.170	0.173	0.178	0.170	0.142	0.140	0.137	0.129
65	T112084 Synothele MYG127 NHD	0.162	0.192	0.195	0.203	0.173	0.197	0.203	0.186	0.200
66	T112949 Aname MYG227 NHG	0.153	0.203	0.200	0.197	0.197	0.184	0.200	0.170	0.189
67	T121597 Aname MYG250 NHQ	0.175	0.173	0.175	0.197	0.164	0.132	0.142	0.148	0.126
68	T122062 Aname MYG182 NGX	0.145	0.214	0.216	0.186	0.219	0.175	0.181	0.189	0.184
69	T96570 Aname MYG067 NHF	0.156	0.216	0.219	0.189	0.222	0.178	0.200	0.175	0.181
70	T98759 Aname MYG185 NHK	0.148	0.222	0.225	0.214	0.238	0.211	0.241	0.203	0.200
71	T98900 Aname MYG034 NHJ	0.132	0.195	0.192	0.195	0.197	0.175	0.173	0.175	0.170
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.164	0.214	0.216	0.181	0.214	0.162	0.192	0.178	0.175
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.175	0.167	0.164	0.148	0.175	0.175	0.192	0.184	0.162
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.142	0.200	0.203	0.208	0.203	0.195	0.178	0.186	0.205
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.159	0.162	0.159	0.137	0.162	0.156	0.170	0.170	0.151
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.101	0.203	0.197	0.192	0.208	0.203	0.197	0.197	0.195
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.110	0.208	0.203	0.205	0.205	0.208	0.205	0.203	0.203
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.162	0.159	0.156	0.137	0.164	0.156	0.175	0.164	0.151
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.156	0.153	0.151	0.134	0.153	0.159	0.170	0.167	0.145
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.156	0.164	0.162	0.140	0.164	0.164	0.173	0.170	0.156
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.156	0.159	0.156	0.137	0.159	0.159	0.167	0.167	0.153
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.156	0.159	0.156	0.137	0.159	0.159	0.170	0.170	0.151
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.159	0.164	0.162	0.142	0.164	0.164	0.164	0.170	0.153
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.162	0.162	0.159	0.140	0.162	0.162	0.173	0.164	0.148

		37	38	39	40	41	42	43	44	45
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.156	0.162	0.159	0.137	0.162	0.162	0.173	0.173	0.153
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.003	0.205	0.200	0.192	0.211	0.181	0.195	0.178	0.189
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.003	0.205	0.200	0.192	0.211	0.181	0.195	0.178	0.189
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.005	0.208	0.203	0.189	0.214	0.184	0.197	0.181	0.186
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.000	0.208	0.203	0.195	0.214	0.184	0.197	0.181	0.192
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.025	0.205	0.200	0.189	0.205	0.184	0.195	0.173	0.175
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.022	0.205	0.200	0.192	0.205	0.181	0.192	0.173	0.178
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.156	0.164	0.162	0.140	0.164	0.162	0.170	0.164	0.153
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.203	0.121	0.123	0.197	0.107	0.159	0.151	0.142	0.148
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.203	0.121	0.123	0.197	0.107	0.159	0.151	0.142	0.148
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.175	0.173	0.175	0.197	0.164	0.132	0.142	0.148	0.126
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.159	0.159	0.156	0.140	0.164	0.159	0.175	0.167	0.153
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.148	0.159	0.156	0.132	0.159	0.156	0.167	0.156	0.145
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.159	0.162	0.159	0.148	0.162	0.159	0.164	0.164	0.156
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.175	0.164	0.156	0.142	0.170	0.162	0.189	0.181	0.164
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.184	0.173	0.164	0.181	0.184	0.000	0.137	0.145	0.134
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.159	0.159	0.156	0.137	0.164	0.159	0.173	0.170	0.156
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.159	0.159	0.156	0.137	0.164	0.159	0.173	0.170	0.156
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.159	0.162	0.159	0.137	0.167	0.156	0.173	0.164	0.151
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.162	0.162	0.159	0.140	0.162	0.159	0.175	0.173	0.159
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.162	0.156	0.153	0.142	0.156	0.164	0.175	0.167	0.151
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.162	0.156	0.159	0.137	0.162	0.167	0.175	0.164	0.148
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.162	0.162	0.159	0.140	0.162	0.159	0.175	0.173	0.159
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.164	0.156	0.159	0.145	0.167	0.162	0.175	0.167	0.145
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.156	0.153	0.156	0.134	0.159	0.162	0.175	0.167	0.148
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.175	0.170	0.173	0.181	0.186	0.148	0.162	0.151	0.140
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.126	0.189	0.186	0.178	0.200	0.178	0.189	0.164	0.159
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.126	0.189	0.186	0.178	0.200	0.178	0.189	0.164	0.159

		37	38	39	40	41	42	43	44	45
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.126	0.189	0.186	0.178	0.200	0.178	0.189	0.164	0.159
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.189	0.178	0.181	0.205	0.178	0.153	0.170	0.145	0.126
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.126	0.189	0.186	0.178	0.200	0.178	0.189	0.164	0.159
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.140	0.195	0.197	0.189	0.200	0.186	0.189	0.167	0.167
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.126	0.189	0.186	0.178	0.200	0.178	0.189	0.164	0.159
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.126	0.203	0.200	0.156	0.208	0.178	0.189	0.178	0.159
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.132	0.195	0.192	0.195	0.197	0.175	0.173	0.175	0.170

		46	47	48	49	50	51	52	53	54
1	PC12	0.020	0.020	0.018	0.020	0.018	0.019	0.019	0.020	0.020
2	PC27	0.021	0.020	0.018	0.020	0.018	0.020	0.020	0.020	0.020
3	PC29	0.021	0.020	0.018	0.020	0.018	0.020	0.020	0.020	0.020
4	PC13	0.020	0.020	0.018	0.020	0.018	0.019	0.019	0.020	0.020
5	PC28	0.020	0.020	0.018	0.020	0.018	0.019	0.019	0.020	0.020
6	PC18	0.020	0.019	0.020	0.021	0.020	0.019	0.019	0.020	0.019
7	PC15	0.019	0.021	0.020	0.019	0.020	0.020	0.019	0.020	0.019
8	PC16	0.019	0.019	0.019	0.020	0.020	0.017	0.017	0.017	0.017
9	PC26	0.019	0.019	0.020	0.020	0.020	0.017	0.017	0.018	0.017
10	NA_N1_AG1	0.021	0.019	0.020	0.020	0.021	0.020	0.019	0.020	0.020
11	NAA_N45_AS38	0.020	0.021	0.019	0.020	0.019	0.021	0.021	0.021	0.021
12	NAB_N46_AS41	0.020	0.020	0.019	0.021	0.019	0.020	0.020	0.020	0.021
13	NAD_N93_AC10	0.021	0.022	0.019	0.021	0.018	0.021	0.021	0.021	0.022
14	NAM_N49_AD14	0.021	0.021	0.020	0.020	0.019	0.020	0.020	0.020	0.021
15	NAO_N22_AD328	0.015	0.021	0.020	0.014	0.021	0.020	0.019	0.020	0.020
16	NAQ_N5_AD352	0.019	0.019	0.019	0.020	0.020	0.016	0.017	0.017	0.017
17	NAW_N6_AD429	0.020	0.019	0.019	0.020	0.019	0.016	0.016	0.016	0.016
18	NAX_N24_AD452	0.014	0.021	0.020	0.015	0.021	0.021	0.021	0.021	0.021
19	NAZ_N6_AD457	0.020	0.018	0.020	0.020	0.019	0.017	0.017	0.018	0.017
20	NB_N16_AH8	0.018	0.021	0.020	0.019	0.021	0.021	0.020	0.020	0.020
21	NBC_N6_AD577	0.019	0.019	0.020	0.020	0.020	0.017	0.017	0.018	0.018
22	NBE_N46_AD583	0.021	0.020	0.020	0.020	0.020	0.021	0.021	0.022	0.022
23	NBM_N4_AD678	0.021	0.019	0.020	0.021	0.021	0.018	0.018	0.018	0.018
24	NBR_N14_AD746	0.020	0.020	0.020	0.021	0.019	0.020	0.020	0.021	0.020
25	NBT_N7_AD748	0.021	0.018	0.020	0.021	0.021	0.011	0.010	0.011	0.011
26	NBU_N15_AD753	0.020	0.020	0.019	0.021	0.020	0.020	0.020	0.020	0.020
27	NBW_N50_AD784	0.021	0.021	0.020	0.021	0.020	0.019	0.019	0.020	0.020
28	NCA_N20_AF78	0.012	0.022	0.021	0.015	0.021	0.021	0.021	0.021	0.021

		46	47	48	49	50	51	52	53	54
29	NCG_N95_I16	0.021	0.021	0.019	0.020	0.019	0.021	0.021	0.021	0.021
30	NCU_N110_O211	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019
31	NCW_N66_O280	0.020	0.019	0.020	0.020	0.020	0.017	0.017	0.017	0.017
32	NCY_N67_O282	0.020	0.020	0.021	0.020	0.021	0.019	0.019	0.019	0.019
33	NCZ_N110_O285	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019
34	NDD_N101_O292	0.020	0.020	0.019	0.020	0.019	0.020	0.020	0.021	0.020
35	NDK_N94_O333	0.020	0.021	0.019	0.020	0.019	0.020	0.020	0.020	0.020
36	NDL_N96_O334	0.021	0.021	0.019	0.020	0.019	0.020	0.020	0.020	0.020
37	NEH_N112_BI22	0.021	0.018	0.021	0.021	0.019	0.015	0.015	0.015	0.015
38	NEM_N43_DW15	0.021	0.021	0.018	0.021	0.020	0.021	0.021	0.021	0.021
39	NEM_N43_AT53	0.021	0.021	0.018	0.021	0.020	0.021	0.021	0.021	0.021
40	NEW_N19_AD381	0.015	0.021	0.020	0.015	0.021	0.020	0.020	0.021	0.021
41	NFN_N43_CG5	0.020	0.021	0.019	0.021	0.020	0.021	0.021	0.022	0.022
42	NFO_N127_CB26	0.020	0.020	0.019	0.021	0.019	0.021	0.021	0.021	0.021
43	NFZ_N122_BV095	0.020	0.021	0.019	0.021	0.020	0.021	0.021	0.021	0.021
44	NGC_N129_CW5	0.021	0.021	0.019	0.021	0.019	0.020	0.020	0.021	0.021
45	NGE_N130_CW14	0.020	0.021	0.018	0.018	0.019	0.021	0.020	0.020	0.020
46	NGN_N19_DC5		0.021	0.020	0.013	0.021	0.020	0.020	0.021	0.020
47	NGS_N136_DG10	0.214		0.021	0.022	0.020	0.019	0.019	0.020	0.020
48	NGV_N35_DW21	0.186	0.195		0.020	0.016	0.021	0.020	0.021	0.020
49	NIG_N22+N23_ID10	0.063	0.216	0.186		0.021	0.020	0.020	0.021	0.020
50	NK_N36_AD110	0.195	0.184	0.101	0.197		0.021	0.020	0.020	0.020
51	NRF_N7_NN11	0.189	0.162	0.192	0.186	0.192		0.005	0.009	0.008
52	NRG_N7_NN15	0.186	0.162	0.189	0.184	0.189	0.008		0.008	0.006
53	NRH_N7_NN16	0.192	0.170	0.192	0.192	0.189	0.030	0.022		0.006
54	NRI_N7_NN17	0.189	0.175	0.189	0.189	0.186	0.022	0.014	0.014	
55	NRJ_N7_NN18	0.189	0.173	0.189	0.189	0.186	0.022	0.014	0.008	0.005
56	NRK_N7_NN20	0.189	0.162	0.184	0.186	0.178	0.033	0.030	0.036	0.038

		46	47	48	49	50	51	52	53	54
57	NRL_N7_NN21	0.195	0.162	0.184	0.192	0.178	0.033	0.030	0.036	0.038
58	NRM_N7_NN37	0.211	0.167	0.197	0.200	0.200	0.060	0.058	0.063	0.066
59	NRO_N7_NN38	0.189	0.156	0.186	0.186	0.175	0.033	0.030	0.036	0.038
60	NRP_N138_NN35	0.156	0.173	0.170	0.164	0.170	0.132	0.126	0.132	0.129
61	NRQ_N138_NN36	0.164	0.173	0.178	0.170	0.178	0.137	0.132	0.129	0.132
62	NRW_N144_OU21	0.162	0.219	0.145	0.189	0.132	0.192	0.192	0.192	0.192
63	NY_N37_AR64	0.189	0.205	0.093	0.186	0.079	0.184	0.181	0.178	0.178
64	T101209 Kwonkan MYG175 NHP	0.162	0.225	0.145	0.186	0.132	0.186	0.186	0.186	0.186
65	T112084 Synothele MYG127 NHD	0.181	0.175	0.167	0.186	0.178	0.151	0.153	0.153	0.153
66	T112949 Aname MYG227 NHG	0.173	0.167	0.178	0.184	0.197	0.153	0.156	0.162	0.156
67	T121597 Aname MYG250 NHQ	0.184	0.195	0.134	0.186	0.142	0.178	0.178	0.181	0.181
68	T122062 Aname MYG182 NGX	0.184	0.173	0.186	0.195	0.170	0.148	0.145	0.153	0.153
69	T96570 Aname MYG067 NHF	0.178	0.189	0.184	0.186	0.192	0.156	0.159	0.167	0.167
70	T98759 Aname MYG185 NHK	0.197	0.145	0.205	0.208	0.186	0.162	0.159	0.164	0.162
71	T98900 Aname MYG034 NHJ	0.178	0.170	0.162	0.192	0.162	0.126	0.121	0.126	0.123
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.164	0.170	0.181	0.167	0.181	0.164	0.164	0.175	0.170
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.132	0.205	0.186	0.129	0.203	0.181	0.178	0.184	0.184
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.205	0.148	0.189	0.208	0.192	0.137	0.137	0.145	0.145
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.137	0.178	0.156	0.132	0.184	0.162	0.164	0.173	0.170
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.192	0.134	0.189	0.197	0.205	0.047	0.038	0.049	0.047
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.197	0.142	0.192	0.200	0.203	0.055	0.047	0.058	0.055
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.140	0.181	0.159	0.132	0.195	0.164	0.167	0.175	0.173
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.140	0.178	0.153	0.129	0.192	0.162	0.164	0.173	0.170
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.142	0.181	0.164	0.132	0.195	0.162	0.164	0.173	0.170
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.142	0.181	0.159	0.132	0.192	0.162	0.164	0.173	0.170
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.140	0.178	0.159	0.129	0.192	0.162	0.164	0.173	0.170
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.142	0.186	0.159	0.132	0.186	0.164	0.167	0.175	0.173
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.145	0.175	0.156	0.134	0.195	0.164	0.167	0.175	0.173

		46	47	48	49	50	51	52	53	54
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.140	0.178	0.162	0.129	0.192	0.162	0.164	0.173	0.170
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.200	0.129	0.195	0.197	0.159	0.082	0.085	0.093	0.093
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.200	0.129	0.195	0.197	0.159	0.082	0.085	0.093	0.093
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.197	0.132	0.192	0.195	0.162	0.079	0.082	0.090	0.090
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.203	0.132	0.197	0.200	0.162	0.085	0.088	0.096	0.096
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.197	0.140	0.203	0.189	0.175	0.079	0.082	0.096	0.096
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.200	0.137	0.203	0.192	0.173	0.079	0.082	0.096	0.096
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.142	0.175	0.164	0.134	0.195	0.167	0.170	0.178	0.175
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.167	0.214	0.159	0.181	0.186	0.186	0.186	0.192	0.189
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.167	0.214	0.159	0.181	0.186	0.186	0.186	0.192	0.189
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.184	0.195	0.134	0.186	0.142	0.178	0.178	0.181	0.181
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.137	0.178	0.162	0.137	0.200	0.170	0.173	0.181	0.178
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.134	0.181	0.156	0.126	0.178	0.164	0.167	0.175	0.173
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.153	0.181	0.164	0.142	0.192	0.173	0.175	0.186	0.181
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.148	0.192	0.170	0.140	0.195	0.178	0.181	0.192	0.186
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.189	0.186	0.156	0.192	0.151	0.195	0.195	0.197	0.200
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.140	0.184	0.164	0.134	0.197	0.164	0.167	0.175	0.173
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.140	0.184	0.164	0.134	0.197	0.164	0.167	0.175	0.173
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.137	0.178	0.162	0.132	0.195	0.162	0.164	0.173	0.170
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.142	0.186	0.167	0.137	0.200	0.167	0.170	0.178	0.175
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.145	0.178	0.156	0.134	0.192	0.167	0.170	0.178	0.175
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.142	0.181	0.156	0.132	0.195	0.162	0.164	0.173	0.170
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.142	0.186	0.167	0.137	0.200	0.167	0.170	0.178	0.175
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.148	0.178	0.162	0.132	0.195	0.164	0.167	0.175	0.173
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.140	0.178	0.153	0.126	0.189	0.156	0.159	0.167	0.167
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.175	0.214	0.164	0.170	0.162	0.173	0.170	0.175	0.175
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.173	0.159	0.162	0.186	0.159	0.110	0.101	0.104	0.104
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.173	0.159	0.162	0.186	0.159	0.110	0.101	0.104	0.104

		46	47	48	49	50	51	52	53	54
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.173	0.159	0.162	0.186	0.159	0.110	0.101	0.104	0.104
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.192	0.214	0.162	0.189	0.156	0.189	0.189	0.184	0.184
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.173	0.159	0.162	0.186	0.159	0.110	0.101	0.104	0.104
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.175	0.167	0.167	0.189	0.164	0.129	0.121	0.123	0.123
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.173	0.159	0.162	0.186	0.159	0.110	0.101	0.104	0.104
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.164	0.156	0.173	0.167	0.173	0.118	0.121	0.129	0.129
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.178	0.170	0.162	0.192	0.162	0.126	0.121	0.126	0.123

		55	56	57	58	59	60	61	62	63
1	PC12	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.018	0.018
2	PC27	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.019
3	PC29	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.018
4	PC13	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.019
5	PC28	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.019
6	PC18	0.020	0.020	0.019	0.020	0.019	0.020	0.020	0.020	0.020
7	PC15	0.020	0.020	0.020	0.020	0.020	0.019	0.020	0.019	0.020
8	PC16	0.017	0.016	0.017	0.017	0.016	0.016	0.017	0.020	0.020
9	PC26	0.018	0.017	0.017	0.018	0.017	0.017	0.017	0.020	0.020
10	NA_N1_AG1	0.020	0.019	0.019	0.020	0.019	0.020	0.020	0.021	0.020
11	NAA_N45_AS38	0.021	0.021	0.020	0.021	0.020	0.021	0.021	0.018	0.019
12	NAB_N46_AS41	0.021	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.019
13	NAD_N93_AC10	0.022	0.022	0.021	0.022	0.022	0.021	0.021	0.019	0.019
14	NAM_N49_AD14	0.020	0.021	0.021	0.021	0.021	0.021	0.021	0.020	0.019
15	NAO_N22_AD328	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.020	0.021
16	NAQ_N5_AD352	0.017	0.017	0.017	0.017	0.017	0.018	0.018	0.020	0.020
17	NAW_N6_AD429	0.016	0.015	0.015	0.017	0.015	0.017	0.017	0.020	0.020
18	NAX_N24_AD452	0.021	0.021	0.021	0.021	0.021	0.019	0.020	0.020	0.020
19	NAZ_N6_AD457	0.017	0.017	0.017	0.018	0.017	0.017	0.018	0.020	0.020
20	NB_N16_AH8	0.020	0.021	0.021	0.020	0.021	0.020	0.020	0.021	0.020
21	NBC_N6_AD577	0.017	0.017	0.017	0.018	0.017	0.017	0.017	0.020	0.020
22	NBE_N46_AD583	0.022	0.022	0.021	0.022	0.022	0.020	0.020	0.019	0.019
23	NBM_N4_AD678	0.018	0.018	0.018	0.019	0.018	0.020	0.020	0.020	0.021
24	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
25	NBT_N7_AD748	0.011	0.011	0.011	0.013	0.011	0.018	0.018	0.021	0.021
26	NBU_N15_AD753	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.019	0.020
27	NBW_N50_AD784	0.020	0.020	0.020	0.020	0.019	0.021	0.021	0.020	0.020
28	NCA_N20_AF78	0.021	0.021	0.021	0.022	0.021	0.020	0.020	0.020	0.021

		55	56	57	58	59	60	61	62	63
29	NCG_N95_I16	0.021	0.020	0.020	0.021	0.020	0.020	0.021	0.019	0.020
30	NCU_N110_O211	0.019	0.019	0.019	0.019	0.019	0.019	0.020	0.021	0.020
31	NCW_N66_O280	0.017	0.017	0.017	0.018	0.017	0.019	0.019	0.021	0.020
32	NCY_N67_O282	0.019	0.019	0.019	0.019	0.018	0.019	0.019	0.022	0.021
33	NCZ_N110_O285	0.019	0.019	0.019	0.019	0.019	0.018	0.019	0.020	0.019
34	NDD_N101_O292	0.020	0.020	0.020	0.020	0.020	0.019	0.020	0.020	0.020
35	NDK_N94_O333	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.020
36	NDL_N96_O334	0.020	0.020	0.020	0.021	0.020	0.021	0.021	0.018	0.019
37	NEH_N112_BI22	0.015	0.015	0.015	0.016	0.015	0.018	0.018	0.020	0.020
38	NEM_N43_DW15	0.021	0.021	0.021	0.021	0.021	0.021	0.021	0.020	0.020
39	NEM_N43_AT53	0.021	0.021	0.021	0.021	0.021	0.021	0.021	0.020	0.020
40	NEW_N19_AD381	0.021	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.021
41	NFN_N43_CG5	0.022	0.021	0.021	0.021	0.021	0.021	0.021	0.020	0.020
42	NFO_N127_CB26	0.021	0.021	0.020	0.022	0.021	0.019	0.020	0.018	0.019
43	NFZ_N122_BV095	0.021	0.021	0.021	0.021	0.021	0.020	0.020	0.018	0.019
44	NGC_N129_CW5	0.021	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.020
45	NGE_N130_CW14	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.018
46	NGN_N19_DC5	0.020	0.020	0.021	0.021	0.020	0.019	0.019	0.019	0.020
47	NGS_N136_DG10	0.020	0.019	0.019	0.020	0.019	0.020	0.020	0.022	0.021
48	NGV_N35_DW21	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.015
49	NIG_N22+N23_ID10	0.020	0.020	0.021	0.021	0.020	0.019	0.020	0.020	0.020
50	NK_N36_AD110	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.014
51	NRF_N7_NN11	0.008	0.009	0.009	0.012	0.009	0.018	0.018	0.021	0.020
52	NRG_N7_NN15	0.006	0.009	0.009	0.012	0.009	0.017	0.018	0.021	0.020
53	NRH_N7_NN16	0.005	0.010	0.010	0.013	0.010	0.018	0.018	0.021	0.020
54	NRI_N7_NN17	0.004	0.010	0.010	0.013	0.010	0.018	0.018	0.021	0.020
55	NRJ_N7_NN18		0.009	0.009	0.012	0.009	0.018	0.018	0.020	0.020
56	NRK_N7_NN20	0.033		0.004	0.011	0.004	0.018	0.018	0.020	0.020

		55	56	57	58	59	60	61	62	63
57	NRL_N7_NN21	0.033	0.005		0.012	0.004	0.018	0.018	0.020	0.020
58	NRM_N7_NN37	0.060	0.049	0.055		0.011	0.019	0.019	0.021	0.021
59	NRO_N7_NN38	0.033	0.005	0.005	0.049		0.018	0.018	0.021	0.020
60	NRP_N138_NN35	0.129	0.137	0.137	0.151	0.137		0.005	0.020	0.019
61	NRQ_N138_NN36	0.132	0.142	0.142	0.156	0.142	0.008		0.020	0.019
62	NRW_N144_OU21	0.189	0.189	0.189	0.208	0.192	0.173	0.181		0.019
63	NY_N37_AR64	0.175	0.178	0.178	0.197	0.181	0.162	0.164	0.148	
64	T101209 Kwonkan MYG175 NHP	0.184	0.184	0.184	0.203	0.186	0.167	0.175	0.005	0.148
65	T112084 Synothele MYG127 NHD	0.151	0.148	0.153	0.148	0.148	0.145	0.153	0.195	0.184
66	T112949 Aname MYG227 NHG	0.159	0.151	0.156	0.151	0.156	0.137	0.134	0.195	0.186
67	T121597 Aname MYG250 NHQ	0.178	0.170	0.175	0.170	0.173	0.162	0.170	0.110	0.137
68	T122062 Aname MYG182 NGX	0.151	0.148	0.142	0.162	0.148	0.156	0.162	0.192	0.159
69	T96570 Aname MYG067 NHF	0.164	0.148	0.153	0.164	0.153	0.151	0.156	0.184	0.192
70	T98759 Aname MYG185 NHK	0.159	0.170	0.170	0.164	0.170	0.175	0.184	0.203	0.197
71	T98900 Aname MYG034 NHJ	0.123	0.110	0.110	0.129	0.115	0.115	0.115	0.181	0.156
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.173	0.178	0.178	0.175	0.178	0.153	0.162	0.181	0.178
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.186	0.195	0.189	0.200	0.189	0.175	0.170	0.192	0.181
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.142	0.140	0.134	0.148	0.137	0.167	0.173	0.186	0.197
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.170	0.184	0.178	0.186	0.178	0.162	0.162	0.181	0.164
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.047	0.047	0.047	0.063	0.047	0.137	0.137	0.195	0.192
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.055	0.049	0.055	0.049	0.049	0.151	0.151	0.211	0.189
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.173	0.186	0.181	0.189	0.181	0.167	0.167	0.189	0.170
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.170	0.178	0.173	0.184	0.173	0.162	0.162	0.189	0.164
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.170	0.184	0.178	0.184	0.178	0.164	0.164	0.192	0.170
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.170	0.184	0.178	0.184	0.178	0.164	0.164	0.186	0.164
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.170	0.184	0.178	0.184	0.178	0.162	0.162	0.189	0.164
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.173	0.186	0.181	0.186	0.181	0.164	0.164	0.181	0.164
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.173	0.181	0.175	0.184	0.175	0.167	0.167	0.189	0.170

		55	56	57	58	59	60	61	62	63
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.170	0.184	0.178	0.184	0.178	0.162	0.162	0.192	0.167
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.090	0.088	0.082	0.104	0.082	0.126	0.126	0.184	0.173
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.090	0.088	0.082	0.104	0.082	0.126	0.126	0.184	0.173
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.088	0.085	0.085	0.101	0.085	0.123	0.123	0.181	0.170
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.093	0.090	0.085	0.107	0.085	0.129	0.129	0.186	0.175
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.093	0.085	0.079	0.101	0.079	0.123	0.123	0.181	0.184
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.093	0.085	0.079	0.101	0.079	0.121	0.121	0.181	0.184
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.175	0.189	0.184	0.189	0.184	0.170	0.170	0.186	0.173
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.192	0.189	0.195	0.192	0.192	0.178	0.184	0.159	0.170
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.192	0.189	0.195	0.192	0.192	0.178	0.184	0.159	0.170
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.178	0.170	0.175	0.170	0.173	0.162	0.170	0.110	0.137
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.178	0.186	0.181	0.186	0.181	0.170	0.170	0.195	0.173
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.173	0.181	0.175	0.181	0.175	0.156	0.156	0.173	0.156
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.184	0.186	0.181	0.181	0.181	0.162	0.162	0.186	0.167
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.189	0.200	0.195	0.195	0.195	0.186	0.186	0.197	0.175
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.200	0.195	0.189	0.219	0.195	0.164	0.167	0.145	0.151
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.173	0.186	0.181	0.186	0.181	0.167	0.167	0.192	0.170
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.173	0.186	0.181	0.186	0.181	0.167	0.167	0.192	0.170
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.170	0.184	0.178	0.186	0.178	0.164	0.164	0.189	0.170
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.175	0.189	0.184	0.189	0.184	0.167	0.167	0.195	0.173
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.175	0.181	0.175	0.184	0.178	0.167	0.167	0.192	0.167
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.170	0.178	0.173	0.178	0.173	0.164	0.170	0.189	0.173
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.175	0.189	0.184	0.189	0.184	0.167	0.167	0.195	0.173
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.173	0.181	0.175	0.175	0.175	0.164	0.170	0.192	0.173
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.164	0.178	0.173	0.178	0.173	0.162	0.167	0.186	0.167
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.175	0.175	0.170	0.197	0.173	0.178	0.186	0.137	0.181
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.101	0.096	0.096	0.118	0.096	0.112	0.115	0.186	0.175
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.101	0.096	0.096	0.118	0.096	0.112	0.115	0.186	0.175

		55	56	57	58	59	60	61	62	63
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.101	0.096	0.096	0.118	0.096	0.112	0.115	0.186	0.175
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.181	0.186	0.181	0.214	0.184	0.200	0.203	0.134	0.156
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.101	0.096	0.096	0.118	0.096	0.112	0.115	0.186	0.175
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.121	0.112	0.118	0.126	0.112	0.115	0.118	0.189	0.178
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.101	0.096	0.096	0.118	0.096	0.112	0.115	0.186	0.175
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.126	0.115	0.115	0.140	0.115	0.121	0.126	0.175	0.189
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.123	0.110	0.110	0.129	0.115	0.115	0.115	0.181	0.156

		64	65	66	67	68	69	70	71	72
1	PC12	0.018	0.020	0.020	0.017	0.020	0.020	0.021	0.020	0.020
2	PC27	0.018	0.020	0.020	0.017	0.020	0.021	0.021	0.020	0.020
3	PC29	0.018	0.020	0.020	0.018	0.020	0.020	0.021	0.020	0.020
4	PC13	0.018	0.020	0.020	0.018	0.020	0.020	0.020	0.020	0.020
5	PC28	0.018	0.020	0.020	0.018	0.020	0.020	0.021	0.020	0.020
6	PC18	0.020	0.020	0.020	0.020	0.020	0.019	0.020	0.020	0.020
7	PC15	0.019	0.021	0.020	0.019	0.020	0.020	0.021	0.020	0.018
8	PC16	0.020	0.018	0.018	0.020	0.019	0.019	0.020	0.015	0.019
9	PC26	0.020	0.020	0.019	0.020	0.018	0.019	0.019	0.016	0.020
10	NA_N1_AG1	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.019	0.019
11	NAA_N45_AS38	0.018	0.021	0.021	0.017	0.020	0.021	0.022	0.020	0.019
12	NAB_N46_AS41	0.017	0.020	0.020	0.018	0.021	0.020	0.022	0.019	0.020
13	NAD_N93_AC10	0.018	0.021	0.021	0.018	0.021	0.022	0.023	0.021	0.021
14	NAM_N49_AD14	0.019	0.020	0.022	0.019	0.021	0.021	0.021	0.020	0.021
15	NAO_N22_AD328	0.020	0.020	0.020	0.019	0.020	0.020	0.021	0.020	0.020
16	NAQ_N5_AD352	0.020	0.019	0.018	0.019	0.019	0.018	0.018	0.017	0.018
17	NAW_N6_AD429	0.020	0.019	0.019	0.020	0.019	0.019	0.019	0.012	0.020
18	NAX_N24_AD452	0.020	0.020	0.020	0.019	0.020	0.019	0.021	0.020	0.019
19	NAZ_N6_AD457	0.020	0.019	0.019	0.020	0.020	0.019	0.018	0.015	0.020
20	NB_N16_AH8	0.021	0.019	0.020	0.020	0.021	0.021	0.020	0.020	0.019
21	NBC_N6_AD577	0.020	0.019	0.019	0.020	0.020	0.019	0.019	0.014	0.019
22	NBE_N46_AD583	0.019	0.021	0.020	0.019	0.020	0.021	0.021	0.021	0.019
23	NBM_N4_AD678	0.020	0.019	0.020	0.020	0.019	0.019	0.020	0.019	0.020
24	NBR_N14_AD746	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
25	NBT_N7_AD748	0.021	0.019	0.019	0.020	0.019	0.019	0.020	0.017	0.020
26	NBU_N15_AD753	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.020	0.020
27	NBW_N50_AD784	0.020	0.021	0.020	0.020	0.021	0.021	0.021	0.020	0.021
28	NCA_N20_AF78	0.020	0.021	0.020	0.020	0.021	0.021	0.021	0.020	0.020

		64	65	66	67	68	69	70	71	72
29	NCG_N95_I16	0.019	0.020	0.020	0.017	0.020	0.020	0.022	0.020	0.020
30	NCU_N110_O211	0.020	0.019	0.019	0.020	0.018	0.019	0.020	0.020	0.020
31	NCW_N66_O280	0.020	0.018	0.018	0.020	0.018	0.019	0.020	0.018	0.019
32	NCY_N67_O282	0.022	0.020	0.020	0.021	0.019	0.019	0.020	0.019	0.020
33	NCZ_N110_O285	0.020	0.020	0.019	0.020	0.018	0.019	0.019	0.019	0.020
34	NDD_N101_O292	0.020	0.019	0.019	0.020	0.019	0.019	0.020	0.020	0.020
35	NDK_N94_O333	0.018	0.021	0.020	0.018	0.020	0.020	0.021	0.020	0.021
36	NDL_N96_O334	0.018	0.021	0.021	0.017	0.020	0.021	0.021	0.020	0.020
37	NEH_N112_BI22	0.020	0.019	0.019	0.020	0.018	0.019	0.019	0.018	0.019
38	NEM_N43_DW15	0.020	0.021	0.021	0.020	0.021	0.022	0.022	0.021	0.021
39	NEM_N43_AT53	0.020	0.021	0.021	0.020	0.022	0.022	0.022	0.021	0.022
40	NEW_N19_AD381	0.020	0.021	0.021	0.021	0.020	0.020	0.021	0.021	0.020
41	NFN_N43_CG5	0.020	0.020	0.021	0.019	0.022	0.022	0.022	0.021	0.021
42	NFO_N127_CB26	0.018	0.021	0.020	0.018	0.020	0.020	0.021	0.020	0.019
43	NFZ_N122_BV095	0.018	0.021	0.021	0.018	0.020	0.021	0.022	0.020	0.021
44	NGC_N129_CW5	0.018	0.020	0.020	0.019	0.020	0.020	0.021	0.020	0.020
45	NGE_N130_CW14	0.018	0.021	0.020	0.017	0.020	0.020	0.021	0.020	0.020
46	NGN_N19_DC5	0.019	0.020	0.020	0.020	0.020	0.020	0.021	0.020	0.019
47	NGS_N136_DG10	0.022	0.020	0.020	0.021	0.020	0.020	0.018	0.020	0.020
48	NGV_N35_DW21	0.018	0.020	0.020	0.018	0.020	0.020	0.021	0.019	0.020
49	NIG_N22+N23_ID10	0.020	0.020	0.020	0.020	0.021	0.020	0.021	0.021	0.020
50	NK_N36_AD110	0.018	0.020	0.021	0.018	0.020	0.021	0.020	0.019	0.020
51	NRF_N7_NN11	0.020	0.019	0.019	0.020	0.019	0.019	0.019	0.017	0.019
52	NRG_N7_NN15	0.020	0.019	0.019	0.020	0.018	0.019	0.019	0.017	0.019
53	NRH_N7_NN16	0.020	0.019	0.019	0.020	0.019	0.020	0.019	0.017	0.020
54	NRI_N7_NN17	0.020	0.019	0.019	0.020	0.019	0.020	0.019	0.017	0.020
55	NRJ_N7_NN18	0.020	0.019	0.019	0.020	0.019	0.019	0.019	0.017	0.020
56	NRK_N7_NN20	0.020	0.019	0.019	0.020	0.019	0.019	0.020	0.016	0.020

		64	65	66	67	68	69	70	71	72
57	NRL_N7_NN21	0.020	0.019	0.019	0.020	0.018	0.019	0.020	0.016	0.020
58	NRM_N7_NN37	0.021	0.019	0.019	0.020	0.019	0.019	0.019	0.018	0.020
59	NRO_N7_NN38	0.020	0.019	0.019	0.020	0.019	0.019	0.020	0.017	0.020
60	NRP_N138_NN35	0.020	0.018	0.018	0.019	0.019	0.019	0.020	0.017	0.019
61	NRQ_N138_NN36	0.020	0.019	0.018	0.020	0.019	0.019	0.020	0.017	0.019
62	NRW_N144_OU21	0.004	0.021	0.021	0.016	0.021	0.020	0.021	0.020	0.020
63	NY_N37_AR64	0.019	0.020	0.020	0.018	0.019	0.021	0.021	0.019	0.020
64	T101209 Kwonkan MYG175 NHP		0.020	0.021	0.016	0.021	0.020	0.021	0.020	0.020
65	T112084 Synothele MYG127 NHD	0.189		0.018	0.020	0.020	0.018	0.019	0.019	0.020
66	T112949 Aname MYG227 NHG	0.192	0.145		0.020	0.019	0.017	0.020	0.019	0.019
67	T121597 Aname MYG250 NHQ	0.110	0.189	0.173		0.020	0.020	0.021	0.019	0.019
68	T122062 Aname MYG182 NGX	0.192	0.181	0.156	0.181		0.018	0.020	0.019	0.020
69	T96570 Aname MYG067 NHF	0.178	0.134	0.118	0.184	0.137		0.020	0.019	0.020
70	T98759 Aname MYG185 NHK	0.205	0.164	0.173	0.205	0.189	0.186		0.019	0.020
71	T98900 Aname MYG034 NHJ	0.175	0.148	0.151	0.164	0.162	0.153	0.164		0.020
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.178	0.184	0.148	0.156	0.173	0.173	0.189	0.175	
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.186	0.173	0.178	0.167	0.181	0.178	0.214	0.173	0.164
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.189	0.162	0.178	0.184	0.153	0.153	0.184	0.156	0.189
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.175	0.159	0.156	0.142	0.159	0.175	0.181	0.178	0.145
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.195	0.156	0.151	0.186	0.159	0.164	0.170	0.126	0.175
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.211	0.162	0.148	0.178	0.156	0.170	0.173	0.137	0.178
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.184	0.159	0.159	0.148	0.164	0.167	0.189	0.186	0.148
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.184	0.156	0.156	0.145	0.156	0.175	0.195	0.173	0.153
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.186	0.151	0.153	0.151	0.164	0.170	0.189	0.181	0.153
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.181	0.151	0.153	0.145	0.159	0.170	0.189	0.181	0.153
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.184	0.153	0.156	0.145	0.159	0.173	0.186	0.178	0.151
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.175	0.159	0.151	0.148	0.162	0.175	0.189	0.181	0.153
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.184	0.153	0.153	0.142	0.162	0.170	0.192	0.178	0.156

		64	65	66	67	68	69	70	71	72
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.186	0.153	0.156	0.148	0.162	0.173	0.186	0.178	0.151
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.178	0.159	0.151	0.173	0.142	0.153	0.145	0.129	0.162
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.178	0.159	0.151	0.173	0.142	0.153	0.145	0.129	0.162
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.175	0.156	0.148	0.170	0.145	0.151	0.142	0.126	0.159
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.181	0.162	0.153	0.175	0.145	0.156	0.148	0.132	0.164
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.175	0.162	0.142	0.170	0.142	0.156	0.162	0.132	0.164
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.175	0.159	0.140	0.173	0.140	0.153	0.159	0.129	0.167
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.181	0.153	0.159	0.148	0.167	0.173	0.189	0.178	0.156
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.153	0.167	0.186	0.134	0.211	0.178	0.227	0.164	0.184
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.153	0.167	0.186	0.134	0.211	0.178	0.227	0.164	0.184
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.110	0.189	0.173	0.000	0.181	0.184	0.205	0.164	0.156
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.189	0.153	0.153	0.153	0.167	0.162	0.192	0.181	0.151
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.167	0.148	0.145	0.137	0.156	0.164	0.181	0.178	0.153
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.181	0.159	0.162	0.142	0.167	0.173	0.197	0.175	0.159
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.192	0.175	0.175	0.159	0.178	0.184	0.195	0.189	0.167
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.142	0.197	0.184	0.132	0.175	0.178	0.211	0.175	0.162
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.186	0.153	0.156	0.151	0.164	0.167	0.192	0.184	0.151
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.186	0.153	0.156	0.151	0.164	0.167	0.192	0.184	0.151
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.184	0.153	0.156	0.148	0.164	0.164	0.186	0.181	0.145
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.189	0.156	0.159	0.148	0.167	0.170	0.195	0.186	0.153
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.186	0.153	0.153	0.148	0.164	0.170	0.192	0.175	0.156
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.184	0.148	0.153	0.142	0.159	0.167	0.192	0.181	0.156
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.189	0.156	0.159	0.148	0.167	0.170	0.195	0.186	0.153
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.186	0.156	0.164	0.148	0.156	0.164	0.186	0.175	0.148
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.181	0.151	0.159	0.142	0.151	0.167	0.181	0.181	0.148
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.132	0.203	0.189	0.140	0.175	0.181	0.195	0.189	0.208
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.181	0.153	0.156	0.173	0.162	0.159	0.153	0.055	0.175
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.181	0.153	0.156	0.173	0.162	0.159	0.153	0.055	0.175

		64	65	66	67	68	69	70	71	72
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.181	0.153	0.156	0.173	0.162	0.159	0.153	0.055	0.175
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.132	0.200	0.197	0.123	0.181	0.203	0.208	0.170	0.189
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.181	0.153	0.156	0.173	0.162	0.159	0.153	0.055	0.175
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.184	0.153	0.153	0.164	0.153	0.151	0.164	0.044	0.175
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.181	0.153	0.156	0.173	0.162	0.159	0.153	0.055	0.175
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.173	0.151	0.156	0.170	0.178	0.159	0.151	0.079	0.162
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.175	0.148	0.151	0.164	0.162	0.153	0.164	0.000	0.175

		73	74	75	76	77	78	79	80	81
1	PC12	0.018	0.021	0.017	0.020	0.020	0.018	0.018	0.018	0.017
2	PC27	0.019	0.021	0.017	0.020	0.020	0.018	0.018	0.018	0.018
3	PC29	0.019	0.020	0.018	0.020	0.020	0.018	0.018	0.018	0.018
4	PC13	0.018	0.020	0.017	0.020	0.020	0.017	0.018	0.018	0.018
5	PC28	0.019	0.020	0.018	0.020	0.020	0.018	0.018	0.018	0.018
6	PC18	0.018	0.019	0.018	0.019	0.020	0.018	0.018	0.018	0.018
7	PC15	0.018	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.019
8	PC16	0.020	0.019	0.020	0.016	0.017	0.020	0.019	0.020	0.020
9	PC26	0.020	0.020	0.020	0.017	0.017	0.020	0.020	0.020	0.020
10	NA_N1_AG1	0.020	0.021	0.020	0.019	0.020	0.020	0.020	0.020	0.020
11	NAA_N45_AS38	0.019	0.020	0.019	0.020	0.021	0.019	0.019	0.019	0.019
12	NAB_N46_AS41	0.019	0.021	0.019	0.021	0.021	0.020	0.019	0.020	0.019
13	NAD_N93_AC10	0.021	0.021	0.020	0.022	0.022	0.020	0.020	0.020	0.020
14	NAM_N49_AD14	0.021	0.021	0.020	0.021	0.021	0.020	0.020	0.020	0.020
15	NAO_N22_AD328	0.016	0.021	0.017	0.020	0.020	0.017	0.017	0.017	0.017
16	NAQ_N5_AD352	0.020	0.019	0.019	0.017	0.017	0.019	0.019	0.019	0.019
17	NAW_N6_AD429	0.020	0.019	0.020	0.016	0.017	0.020	0.020	0.020	0.020
18	NAX_N24_AD452	0.018	0.021	0.017	0.020	0.021	0.017	0.017	0.017	0.017
19	NAZ_N6_AD457	0.019	0.019	0.019	0.017	0.018	0.019	0.019	0.019	0.019
20	NB_N16_AH8	0.014	0.021	0.014	0.020	0.020	0.014	0.014	0.014	0.014
21	NBC_N6_AD577	0.020	0.019	0.019	0.017	0.018	0.020	0.019	0.020	0.020
22	NBE_N46_AD583	0.020	0.021	0.019	0.021	0.022	0.019	0.019	0.019	0.019
23	NBM_N4_AD678	0.021	0.000	0.020	0.018	0.018	0.020	0.020	0.020	0.020
24	NBR_N14_AD746	0.020	0.021	0.020	0.019	0.020	0.020	0.020	0.020	0.020
25	NBT_N7_AD748	0.020	0.018	0.019	0.000	0.007	0.020	0.019	0.019	0.019
26	NBU_N15_AD753	0.020	0.020	0.018	0.019	0.020	0.019	0.018	0.019	0.019
27	NBW_N50_AD784	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
28	NCA_N20_AF78	0.018	0.021	0.019	0.021	0.021	0.019	0.019	0.019	0.019

		73	74	75	76	77	78	79	80	81
29	NCG_N95_I16	0.020	0.020	0.019	0.021	0.021	0.020	0.019	0.020	0.019
30	NCU_N110_O211	0.019	0.019	0.018	0.020	0.019	0.018	0.019	0.019	0.019
31	NCW_N66_O280	0.020	0.018	0.019	0.017	0.018	0.018	0.018	0.019	0.018
32	NCY_N67_O282	0.020	0.020	0.020	0.019	0.019	0.020	0.020	0.020	0.020
33	NCZ_N110_O285	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
34	NDD_N101_O292	0.019	0.020	0.018	0.020	0.020	0.018	0.018	0.018	0.018
35	NDK_N94_O333	0.020	0.021	0.020	0.020	0.021	0.020	0.020	0.020	0.020
36	NDL_N96_O334	0.020	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020
37	NEH_N112_BI22	0.020	0.018	0.019	0.016	0.016	0.019	0.019	0.019	0.019
38	NEM_N43_DW15	0.020	0.021	0.019	0.021	0.021	0.019	0.019	0.019	0.019
39	NEM_N43_AT53	0.019	0.021	0.019	0.021	0.021	0.019	0.019	0.019	0.019
40	NEW_N19_AD381	0.019	0.021	0.018	0.021	0.021	0.018	0.018	0.018	0.018
41	NFN_N43_CG5	0.020	0.021	0.019	0.021	0.021	0.019	0.019	0.019	0.019
42	NFO_N127_CB26	0.020	0.021	0.019	0.021	0.021	0.019	0.019	0.019	0.019
43	NFZ_N122_BV095	0.021	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020
44	NGC_N129_CW5	0.020	0.020	0.020	0.021	0.021	0.019	0.020	0.020	0.020
45	NGE_N130_CW14	0.019	0.021	0.019	0.021	0.021	0.019	0.018	0.019	0.019
46	NGN_N19_DC5	0.018	0.021	0.018	0.021	0.021	0.018	0.018	0.018	0.018
47	NGS_N136_DG10	0.021	0.019	0.020	0.018	0.018	0.020	0.020	0.020	0.020
48	NGV_N35_DW21	0.020	0.020	0.019	0.020	0.021	0.019	0.019	0.019	0.019
49	NIG_N22+N23_ID10	0.018	0.021	0.018	0.021	0.021	0.018	0.018	0.018	0.018
50	NK_N36_AD110	0.021	0.021	0.020	0.021	0.021	0.021	0.021	0.021	0.021
51	NRF_N7_NN11	0.020	0.018	0.019	0.011	0.012	0.019	0.019	0.019	0.019
52	NRG_N7_NN15	0.020	0.018	0.019	0.010	0.011	0.020	0.019	0.019	0.019
53	NRH_N7_NN16	0.020	0.018	0.020	0.011	0.012	0.020	0.020	0.020	0.020
54	NRI_N7_NN17	0.020	0.018	0.020	0.011	0.012	0.020	0.020	0.020	0.020
55	NRJ_N7_NN18	0.020	0.018	0.020	0.011	0.012	0.020	0.020	0.020	0.020
56	NRK_N7_NN20	0.021	0.018	0.020	0.011	0.011	0.020	0.020	0.020	0.020

		73	74	75	76	77	78	79	80	81
57	NRL_N7_NN21	0.020	0.018	0.020	0.011	0.012	0.020	0.020	0.020	0.020
58	NRM_N7_NN37	0.021	0.019	0.020	0.013	0.011	0.020	0.020	0.020	0.020
59	NRO_N7_NN38	0.020	0.018	0.020	0.011	0.011	0.020	0.020	0.020	0.020
60	NRP_N138_NN35	0.020	0.020	0.019	0.018	0.019	0.020	0.019	0.019	0.019
61	NRQ_N138_NN36	0.020	0.020	0.019	0.018	0.019	0.020	0.019	0.019	0.019
62	NRW_N144_OU21	0.021	0.020	0.020	0.021	0.021	0.020	0.020	0.021	0.020
63	NY_N37_AR64	0.020	0.021	0.019	0.021	0.020	0.020	0.019	0.020	0.019
64	T101209 Kwonkan MYG175 NHP	0.020	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020
65	T112084 Synothele MYG127 NHD	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
66	T112949 Aname MYG227 NHG	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019
67	T121597 Aname MYG250 NHQ	0.020	0.020	0.018	0.020	0.020	0.019	0.018	0.019	0.018
68	T122062 Aname MYG182 NGX	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
69	T96570 Aname MYG067 NHF	0.020	0.019	0.020	0.019	0.020	0.020	0.020	0.020	0.020
70	T98759 Aname MYG185 NHK	0.021	0.020	0.020	0.020	0.020	0.020	0.021	0.020	0.020
71	T98900 Aname MYG034 NHJ	0.020	0.019	0.020	0.017	0.018	0.020	0.020	0.020	0.020
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.019	0.020	0.018	0.020	0.020	0.019	0.019	0.019	0.019
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163		0.021	0.012	0.020	0.021	0.012	0.012	0.012	0.012
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.208		0.020	0.018	0.018	0.020	0.020	0.020	0.020
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.055	0.189		0.019	0.020	0.006	0.006	0.006	0.005
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.178	0.134	0.164		0.007	0.020	0.019	0.019	0.019
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.195	0.137	0.173	0.019		0.020	0.020	0.020	0.020
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.055	0.189	0.014	0.167	0.175		0.008	0.005	0.005
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.058	0.189	0.014	0.164	0.173	0.022		0.007	0.005
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.055	0.186	0.014	0.164	0.173	0.011	0.016		0.004
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.052	0.186	0.008	0.164	0.173	0.011	0.011	0.005	
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.049	0.186	0.008	0.164	0.173	0.011	0.011	0.005	0.005
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.060	0.195	0.011	0.167	0.175	0.019	0.019	0.014	0.008
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.060	0.186	0.011	0.162	0.170	0.014	0.008	0.014	0.008

		73	74	75	76	77	78	79	80	81
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.052	0.186	0.011	0.164	0.173	0.014	0.014	0.003	0.008
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.173	0.140	0.156	0.099	0.107	0.159	0.153	0.153	0.153
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.173	0.140	0.156	0.099	0.107	0.159	0.153	0.153	0.153
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.175	0.142	0.159	0.096	0.104	0.162	0.156	0.156	0.156
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.175	0.142	0.159	0.101	0.110	0.162	0.156	0.156	0.156
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.175	0.132	0.159	0.090	0.099	0.162	0.151	0.156	0.156
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.178	0.129	0.162	0.090	0.099	0.164	0.153	0.159	0.159
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.055	0.192	0.016	0.164	0.178	0.014	0.019	0.008	0.008
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.167	0.197	0.164	0.197	0.197	0.164	0.156	0.164	0.162
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.167	0.197	0.164	0.197	0.197	0.164	0.156	0.164	0.162
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.167	0.184	0.142	0.186	0.178	0.148	0.145	0.151	0.145
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.058	0.192	0.022	0.167	0.175	0.014	0.019	0.014	0.014
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.060	0.189	0.022	0.167	0.175	0.022	0.025	0.019	0.014
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.063	0.184	0.025	0.173	0.181	0.027	0.027	0.022	0.016
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.071	0.211	0.033	0.184	0.192	0.030	0.041	0.041	0.036
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.175	0.195	0.156	0.203	0.208	0.156	0.159	0.164	0.159
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.049	0.189	0.014	0.167	0.175	0.005	0.016	0.005	0.005
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.049	0.189	0.014	0.167	0.175	0.005	0.016	0.005	0.005
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.049	0.186	0.011	0.164	0.173	0.005	0.019	0.011	0.008
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.052	0.192	0.016	0.170	0.178	0.008	0.019	0.008	0.008
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.058	0.181	0.016	0.164	0.173	0.019	0.014	0.008	0.014
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.060	0.184	0.016	0.164	0.173	0.019	0.008	0.014	0.008
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.052	0.192	0.016	0.170	0.178	0.008	0.019	0.008	0.008
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.063	0.175	0.022	0.167	0.175	0.025	0.019	0.019	0.019
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.058	0.181	0.014	0.167	0.175	0.016	0.016	0.016	0.011
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.178	0.195	0.170	0.189	0.197	0.173	0.173	0.175	0.170
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.175	0.164	0.175	0.107	0.118	0.181	0.170	0.178	0.178
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.175	0.164	0.175	0.107	0.118	0.181	0.170	0.178	0.178

		73	74	75	76	77	78	79	80	81
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.175	0.164	0.175	0.107	0.118	0.181	0.170	0.178	0.178
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.175	0.178	0.170	0.200	0.203	0.175	0.170	0.173	0.170
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.175	0.164	0.175	0.107	0.118	0.181	0.170	0.178	0.178
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.181	0.162	0.181	0.129	0.134	0.184	0.175	0.184	0.184
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.175	0.164	0.175	0.107	0.118	0.181	0.170	0.178	0.178
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.178	0.156	0.162	0.123	0.137	0.170	0.159	0.167	0.167
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.173	0.156	0.178	0.126	0.137	0.186	0.173	0.181	0.181

		82	83	84	85	86	87	88	89	90
1	PC12	0.017	0.017	0.018	0.018	0.019	0.019	0.020	0.020	0.019
2	PC27	0.018	0.018	0.018	0.018	0.020	0.020	0.020	0.020	0.020
3	PC29	0.018	0.018	0.018	0.018	0.019	0.019	0.020	0.020	0.020
4	PC13	0.017	0.018	0.018	0.018	0.019	0.019	0.019	0.019	0.020
5	PC28	0.018	0.018	0.018	0.018	0.019	0.019	0.019	0.019	0.020
6	PC18	0.018	0.018	0.018	0.018	0.019	0.019	0.019	0.019	0.019
7	PC15	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020
8	PC16	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.017	0.017
9	PC26	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.018	0.018
10	NA_N1_AG1	0.020	0.020	0.020	0.020	0.020	0.020	0.019	0.020	0.019
11	NAA_N45_AS38	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020
12	NAB_N46_AS41	0.019	0.020	0.019	0.019	0.021	0.021	0.021	0.021	0.020
13	NAD_N93_AC10	0.020	0.020	0.020	0.020	0.022	0.022	0.022	0.022	0.021
14	NAM_N49_AD14	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.021
15	NAO_N22_AD328	0.017	0.017	0.017	0.017	0.020	0.020	0.020	0.020	0.020
16	NAQ_N5_AD352	0.019	0.019	0.019	0.019	0.017	0.017	0.017	0.017	0.017
17	NAW_N6_AD429	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.017	0.017
18	NAX_N24_AD452	0.017	0.017	0.017	0.017	0.021	0.021	0.021	0.021	0.021
19	NAZ_N6_AD457	0.019	0.019	0.019	0.019	0.017	0.017	0.017	0.017	0.017
20	NB_N16_AH8	0.014	0.014	0.014	0.014	0.020	0.020	0.020	0.020	0.020
21	NBC_N6_AD577	0.019	0.019	0.019	0.019	0.017	0.017	0.017	0.017	0.017
22	NBE_N46_AD583	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.021
23	NBM_N4_AD678	0.020	0.021	0.020	0.020	0.018	0.018	0.018	0.018	0.018
24	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
25	NBT_N7_AD748	0.019	0.020	0.019	0.019	0.016	0.016	0.015	0.016	0.015
26	NBU_N15_AD753	0.019	0.019	0.018	0.019	0.020	0.020	0.020	0.019	0.019
27	NBW_N50_AD784	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
28	NCA_N20_AF78	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.022	0.021

		82	83	84	85	86	87	88	89	90
29	NCG_N95_I16	0.019	0.020	0.019	0.019	0.021	0.021	0.021	0.021	0.020
30	NCU_N110_O211	0.018	0.018	0.019	0.019	0.019	0.019	0.019	0.019	0.018
31	NCW_N66_O280	0.019	0.019	0.018	0.019	0.018	0.018	0.018	0.018	0.017
32	NCY_N67_O282	0.020	0.020	0.020	0.020	0.018	0.018	0.019	0.019	0.019
33	NCZ_N110_O285	0.019	0.019	0.019	0.019	0.018	0.018	0.018	0.018	0.018
34	NDD_N101_O292	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
35	NDK_N94_O333	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
36	NDL_N96_O334	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
37	NEH_N112_BI22	0.019	0.019	0.019	0.019	0.003	0.003	0.004	0.000	0.008
38	NEM_N43_DW15	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.021
39	NEM_N43_AT53	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.021
40	NEW_N19_AD381	0.018	0.018	0.018	0.018	0.021	0.021	0.020	0.021	0.020
41	NFN_N43_CG5	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.021
42	NFO_N127_CB26	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020
43	NFZ_N122_BV095	0.020	0.019	0.020	0.020	0.021	0.021	0.021	0.021	0.021
44	NGC_N129_CW5	0.020	0.020	0.019	0.020	0.020	0.020	0.020	0.020	0.020
45	NGE_N130_CW14	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.021	0.020
46	NGN_N19_DC5	0.018	0.018	0.018	0.018	0.021	0.021	0.021	0.021	0.021
47	NGS_N136_DG10	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.018	0.018
48	NGV_N35_DW21	0.019	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.021
49	NIG_N22+N23_ID10	0.018	0.018	0.018	0.018	0.021	0.021	0.021	0.021	0.020
50	NK_N36_AD110	0.021	0.020	0.021	0.021	0.019	0.019	0.019	0.019	0.020
51	NRF_N7_NN11	0.019	0.019	0.019	0.019	0.014	0.014	0.014	0.015	0.014
52	NRG_N7_NN15	0.019	0.020	0.020	0.019	0.015	0.015	0.014	0.015	0.014
53	NRH_N7_NN16	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015
54	NRI_N7_NN17	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015
55	NRJ_N7_NN18	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015
56	NRK_N7_NN20	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015

		82	83	84	85	86	87	88	89	90
57	NRL_N7_NN21	0.020	0.020	0.020	0.020	0.014	0.014	0.015	0.015	0.014
58	NRM_N7_NN37	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.016	0.016
59	NRO_N7_NN38	0.020	0.020	0.020	0.020	0.014	0.014	0.015	0.015	0.014
60	NRP_N138_NN35	0.019	0.019	0.020	0.019	0.017	0.017	0.017	0.018	0.017
61	NRQ_N138_NN36	0.019	0.019	0.020	0.019	0.017	0.017	0.017	0.018	0.017
62	NRW_N144_OU21	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020
63	NY_N37_AR64	0.019	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020
64	T101209 Kwonkan MYG175 NHP	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
65	T112084 Synothele MYG127 NHD	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
66	T112949 Aname MYG227 NHG	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.018
67	T121597 Aname MYG250 NHQ	0.018	0.019	0.018	0.019	0.020	0.020	0.020	0.020	0.020
68	T122062 Aname MYG182 NGX	0.019	0.019	0.019	0.019	0.018	0.018	0.018	0.018	0.018
69	T96570 Aname MYG067 NHF	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.019
70	T98759 Aname MYG185 NHK	0.020	0.020	0.021	0.020	0.018	0.018	0.018	0.019	0.019
71	T98900 Aname MYG034 NHJ	0.020	0.020	0.020	0.020	0.018	0.018	0.017	0.018	0.018
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.011	0.012	0.012	0.012	0.020	0.020	0.020	0.020	0.020
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.020	0.021	0.020	0.020	0.018	0.018	0.018	0.018	0.018
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.005	0.005	0.005	0.005	0.019	0.019	0.019	0.019	0.019
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.019	0.020	0.019	0.019	0.016	0.016	0.015	0.016	0.015
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.016	0.016
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.005	0.007	0.006	0.006	0.019	0.019	0.019	0.019	0.019
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.005	0.007	0.005	0.006	0.019	0.019	0.019	0.019	0.019
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.004	0.006	0.006	0.003	0.019	0.019	0.019	0.019	0.019
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.004	0.005	0.005	0.005	0.019	0.019	0.019	0.019	0.019
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642		0.006	0.006	0.003	0.019	0.019	0.019	0.019	0.019
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.014		0.007	0.007	0.019	0.019	0.019	0.019	0.019
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.014	0.016		0.007	0.019	0.019	0.019	0.019	0.019

		82	83	84	85	86	87	88	89	90
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.003	0.016	0.016		0.019	0.019	0.019	0.019	0.019
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.153	0.156	0.159	0.153		0.000	0.003	0.003	0.008
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.153	0.156	0.159	0.153	0.000		0.003	0.003	0.008
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.156	0.159	0.162	0.156	0.003	0.003		0.004	0.008
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.156	0.159	0.162	0.156	0.003	0.003	0.005		0.008
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.156	0.156	0.156	0.156	0.022	0.022	0.025	0.025	
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.159	0.159	0.159	0.159	0.019	0.019	0.022	0.022	0.003
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.008	0.016	0.016	0.011	0.153	0.153	0.156	0.156	0.156
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.159	0.167	0.164	0.162	0.200	0.200	0.197	0.203	0.200
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.159	0.167	0.164	0.162	0.200	0.200	0.197	0.203	0.200
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.145	0.148	0.142	0.148	0.173	0.173	0.170	0.175	0.170
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.014	0.019	0.016	0.016	0.156	0.156	0.159	0.159	0.156
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.019	0.022	0.022	0.022	0.145	0.145	0.148	0.148	0.148
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.022	0.025	0.025	0.025	0.156	0.156	0.159	0.159	0.159
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.036	0.044	0.038	0.038	0.173	0.173	0.175	0.175	0.175
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.159	0.164	0.162	0.162	0.181	0.181	0.184	0.184	0.184
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.005	0.014	0.014	0.008	0.156	0.156	0.159	0.159	0.159
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.005	0.014	0.014	0.008	0.156	0.156	0.159	0.159	0.159
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.011	0.016	0.011	0.014	0.156	0.156	0.159	0.159	0.159
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.008	0.016	0.016	0.011	0.159	0.159	0.162	0.162	0.162
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.008	0.022	0.016	0.005	0.159	0.159	0.162	0.162	0.156
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.014	0.016	0.005	0.016	0.159	0.159	0.162	0.162	0.156
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.008	0.016	0.016	0.011	0.159	0.159	0.162	0.162	0.162
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.014	0.027	0.022	0.016	0.162	0.162	0.164	0.164	0.159
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.011	0.019	0.019	0.014	0.153	0.153	0.156	0.156	0.156
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.173	0.170	0.173	0.175	0.173	0.173	0.175	0.175	0.175
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.175	0.175	0.175	0.175	0.123	0.123	0.121	0.126	0.121
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.175	0.175	0.175	0.175	0.123	0.123	0.121	0.126	0.121

		82	83	84	85	86	87	88	89	90
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.175	0.175	0.175	0.175	0.123	0.123	0.121	0.126	0.121
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.167	0.173	0.175	0.170	0.186	0.186	0.189	0.189	0.184
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.175	0.175	0.175	0.175	0.123	0.123	0.121	0.126	0.121
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.181	0.184	0.181	0.181	0.137	0.137	0.134	0.140	0.134
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.175	0.175	0.175	0.175	0.123	0.123	0.121	0.126	0.121
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.164	0.162	0.162	0.164	0.123	0.123	0.121	0.126	0.115
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.178	0.181	0.178	0.178	0.129	0.129	0.126	0.132	0.132

		91	92	93	94	95	96	97	98	99
1	PC12	0.020	0.018	0.018	0.018	0.017	0.018	0.017	0.018	0.018
2	PC27	0.020	0.018	0.018	0.018	0.017	0.018	0.017	0.018	0.018
3	PC29	0.020	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
4	PC13	0.019	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.018
5	PC28	0.019	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.018
6	PC18	0.019	0.018	0.020	0.020	0.020	0.018	0.018	0.018	0.018
7	PC15	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.020
8	PC16	0.017	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
9	PC26	0.018	0.020	0.020	0.020	0.020	0.019	0.019	0.020	0.020
10	NA_N1_AG1	0.019	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.021
11	NAA_N45_AS38	0.020	0.019	0.020	0.020	0.017	0.019	0.019	0.019	0.020
12	NAB_N46_AS41	0.020	0.020	0.019	0.019	0.018	0.020	0.019	0.019	0.020
13	NAD_N93_AC10	0.021	0.020	0.019	0.019	0.018	0.020	0.020	0.020	0.021
14	NAM_N49_AD14	0.021	0.020	0.019	0.019	0.019	0.020	0.020	0.020	0.020
15	NAO_N22_AD328	0.020	0.017	0.020	0.020	0.019	0.017	0.016	0.018	0.018
16	NAQ_N5_AD352	0.017	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
17	NAW_N6_AD429	0.017	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
18	NAX_N24_AD452	0.021	0.017	0.019	0.019	0.019	0.017	0.017	0.018	0.017
19	NAZ_N6_AD457	0.017	0.019	0.020	0.020	0.020	0.019	0.019	0.019	0.019
20	NB_N16_AH8	0.020	0.014	0.020	0.020	0.020	0.013	0.014	0.015	0.015
21	NBC_N6_AD577	0.017	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020
22	NBE_N46_AD583	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.019	0.019
23	NBM_N4_AD678	0.018	0.021	0.021	0.021	0.020	0.021	0.020	0.020	0.021
24	NBR_N14_AD746	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.020
25	NBT_N7_AD748	0.015	0.019	0.021	0.021	0.020	0.020	0.020	0.020	0.020
26	NBU_N15_AD753	0.019	0.019	0.021	0.021	0.019	0.019	0.019	0.019	0.018
27	NBW_N50_AD784	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.020
28	NCA_N20_AF78	0.021	0.019	0.020	0.020	0.020	0.019	0.018	0.019	0.019

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		91	92	93	94	95	96	97	98	99
57	NRL_N7_NN21	0.014	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.021
58	NRM_N7_NN37	0.016	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.021
59	NRO_N7_NN38	0.014	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.021
60	NRP_N138_NN35	0.017	0.020	0.020	0.020	0.019	0.020	0.019	0.019	0.020
61	NRQ_N138_NN36	0.017	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.020
62	NRW_N144_OU21	0.020	0.020	0.019	0.019	0.016	0.021	0.020	0.020	0.021
63	NY_N37_AR64	0.020	0.020	0.020	0.020	0.018	0.020	0.019	0.020	0.020
64	T101209 Kwonkan MYG175 NHP	0.020	0.020	0.019	0.019	0.016	0.020	0.020	0.020	0.021
65	T112084 Synothele MYG127 NHD	0.019	0.019	0.020	0.020	0.020	0.019	0.019	0.019	0.020
66	T112949 Aname MYG227 NHG	0.018	0.019	0.020	0.020	0.020	0.019	0.018	0.019	0.020
67	T121597 Aname MYG250 NHQ	0.020	0.019	0.018	0.018	0.000	0.019	0.018	0.018	0.019
68	T122062 Aname MYG182 NGX	0.018	0.020	0.021	0.021	0.020	0.020	0.019	0.020	0.020
69	T96570 Aname MYG067 NHF	0.019	0.020	0.020	0.020	0.020	0.019	0.019	0.020	0.020
70	T98759 Aname MYG185 NHK	0.019	0.020	0.022	0.022	0.021	0.021	0.020	0.021	0.021
71	T98900 Aname MYG034 NHJ	0.018	0.020	0.019	0.019	0.019	0.020	0.020	0.020	0.020
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.019	0.020
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.020	0.012	0.020	0.020	0.020	0.012	0.012	0.013	0.013
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.018	0.021	0.021	0.021	0.020	0.021	0.020	0.020	0.021
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.019	0.007	0.019	0.019	0.018	0.008	0.008	0.008	0.009
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.015	0.019	0.021	0.021	0.020	0.020	0.020	0.020	0.020
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.016	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.021
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.019	0.006	0.019	0.019	0.019	0.006	0.008	0.009	0.009
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.019	0.007	0.019	0.019	0.018	0.007	0.008	0.009	0.010
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.019	0.005	0.019	0.019	0.019	0.006	0.007	0.008	0.010
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.019	0.005	0.019	0.019	0.018	0.006	0.006	0.007	0.010
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.019	0.005	0.019	0.019	0.018	0.006	0.007	0.008	0.010
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.019	0.007	0.020	0.020	0.019	0.007	0.008	0.008	0.011
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.019	0.007	0.019	0.019	0.018	0.007	0.008	0.008	0.010

		91	92	93	94	95	96	97	98	99
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.019	0.005	0.019	0.019	0.019	0.007	0.008	0.008	0.010
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.007	0.019	0.021	0.021	0.020	0.019	0.018	0.019	0.020
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.007	0.019	0.021	0.021	0.020	0.019	0.018	0.019	0.020
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.008	0.019	0.021	0.021	0.020	0.019	0.019	0.019	0.020
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.008	0.019	0.021	0.021	0.020	0.019	0.019	0.019	0.020
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.003	0.019	0.021	0.021	0.020	0.019	0.019	0.019	0.020
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818		0.019	0.021	0.021	0.020	0.019	0.019	0.019	0.020
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.159		0.019	0.019	0.019	0.007	0.007	0.008	0.010
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.200	0.162		0.000	0.018	0.019	0.019	0.019	0.019
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.200	0.162	0.000		0.018	0.019	0.019	0.019	0.019
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.173	0.148	0.134	0.134		0.019	0.018	0.018	0.019
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.159	0.016	0.153	0.153	0.153		0.009	0.009	0.011
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.151	0.016	0.162	0.162	0.137	0.027		0.008	0.010
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.162	0.025	0.159	0.159	0.142	0.030	0.025		0.010
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.178	0.038	0.164	0.164	0.159	0.044	0.041	0.041	
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.181	0.162	0.159	0.159	0.132	0.159	0.156	0.159	0.162
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.162	0.008	0.159	0.159	0.151	0.008	0.019	0.022	0.036
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.162	0.008	0.159	0.159	0.151	0.008	0.019	0.022	0.036
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.162	0.014	0.159	0.159	0.148	0.014	0.022	0.025	0.033
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.164	0.011	0.156	0.156	0.148	0.011	0.022	0.025	0.038
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.159	0.016	0.156	0.156	0.148	0.016	0.027	0.030	0.044
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.159	0.016	0.159	0.159	0.142	0.016	0.022	0.025	0.044
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.164	0.011	0.156	0.156	0.148	0.011	0.022	0.025	0.038
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.162	0.022	0.156	0.156	0.148	0.022	0.033	0.030	0.049
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.159	0.019	0.162	0.162	0.142	0.025	0.022	0.027	0.036
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.173	0.175	0.159	0.159	0.140	0.173	0.162	0.173	0.181
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.118	0.175	0.181	0.181	0.173	0.178	0.170	0.178	0.189
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.118	0.175	0.181	0.181	0.173	0.178	0.170	0.178	0.189

		91	92	93	94	95	96	97	98	99
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.118	0.175	0.181	0.181	0.173	0.178	0.170	0.178	0.189
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.186	0.170	0.140	0.140	0.123	0.175	0.162	0.173	0.175
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.118	0.175	0.181	0.181	0.173	0.178	0.170	0.178	0.189
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.132	0.181	0.175	0.175	0.164	0.184	0.178	0.184	0.197
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.118	0.175	0.181	0.181	0.173	0.178	0.170	0.178	0.189
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.118	0.164	0.181	0.181	0.170	0.167	0.170	0.167	0.178
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.129	0.178	0.164	0.164	0.164	0.181	0.178	0.175	0.189

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		100	101	102	103	104	105	106	107	108
57	NRL_N7_NN21	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
58	NRM_N7_NN37	0.022	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
59	NRO_N7_NN38	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
60	NRP_N138_NN35	0.019	0.020	0.020	0.019	0.020	0.020	0.019	0.020	0.019
61	NRQ_N138_NN36	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.020	0.020
62	NRW_N144_OU21	0.018	0.021	0.021	0.020	0.021	0.021	0.020	0.021	0.021
63	NY_N37_AR64	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
64	T101209 Kwonkan MYG175 NHP	0.018	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
65	T112084 Synothele MYG127 NHD	0.021	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
66	T112949 Aname MYG227 NHG	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
67	T121597 Aname MYG250 NHQ	0.018	0.019	0.019	0.019	0.019	0.019	0.018	0.019	0.019
68	T122062 Aname MYG182 NGX	0.020	0.019	0.019	0.019	0.020	0.019	0.019	0.020	0.019
69	T96570 Aname MYG067 NHF	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.020	0.019
70	T98759 Aname MYG185 NHK	0.021	0.021	0.021	0.020	0.021	0.021	0.021	0.021	0.020
71	T98900 Aname MYG034 NHJ	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.019	0.019	0.019	0.018	0.019	0.019	0.019	0.019	0.019
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.020	0.011	0.011	0.011	0.012	0.012	0.012	0.012	0.013
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.021	0.020	0.020	0.020	0.021	0.020	0.020	0.021	0.020
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.019	0.006	0.006	0.005	0.007	0.007	0.007	0.007	0.008
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.021	0.020	0.020	0.019	0.020	0.019	0.019	0.020	0.020
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.019	0.004	0.004	0.004	0.005	0.007	0.007	0.005	0.008
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.019	0.007	0.007	0.007	0.007	0.006	0.005	0.007	0.007
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.019	0.004	0.004	0.005	0.005	0.005	0.006	0.005	0.007
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.019	0.004	0.004	0.005	0.005	0.006	0.005	0.005	0.007
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.019	0.004	0.004	0.005	0.005	0.005	0.006	0.005	0.006
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.019	0.006	0.006	0.007	0.007	0.008	0.007	0.007	0.009
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.019	0.006	0.006	0.005	0.007	0.007	0.004	0.007	0.008

		100	101	102	103	104	105	106	107	108
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.019	0.005	0.005	0.006	0.005	0.004	0.007	0.005	0.007
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.019	0.005	0.005	0.006	0.005	0.007	0.007	0.005	0.008
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.018	0.019	0.019	0.019	0.019	0.019	0.018	0.019	0.019
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.019	0.005	0.005	0.006	0.005	0.007	0.007	0.005	0.008
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.019	0.007	0.007	0.008	0.008	0.009	0.008	0.008	0.009
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.019	0.008	0.008	0.008	0.008	0.009	0.008	0.008	0.009
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.019	0.010	0.010	0.009	0.010	0.011	0.011	0.010	0.011
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329		0.019	0.019	0.019	0.019	0.019	0.020	0.019	0.019
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.159		0.000	0.004	0.003	0.006	0.006	0.003	0.007
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.159	0.000		0.004	0.003	0.006	0.006	0.003	0.007
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.156	0.005	0.005		0.005	0.007	0.007	0.005	0.008
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.159	0.003	0.003	0.008		0.007	0.007	0.000	0.008
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.164	0.014	0.014	0.019	0.016		0.007	0.007	0.007
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.167	0.014	0.014	0.016	0.016	0.016		0.007	0.007
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.159	0.003	0.003	0.008	0.000	0.016	0.016		0.008
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.162	0.019	0.019	0.025	0.022	0.016	0.016	0.022	
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.162	0.016	0.016	0.019	0.019	0.019	0.014	0.019	0.019
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.148	0.175	0.175	0.173	0.178	0.175	0.173	0.178	0.175
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.178	0.181	0.181	0.178	0.184	0.175	0.173	0.184	0.167
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.178	0.181	0.181	0.178	0.184	0.175	0.173	0.184	0.167

		100	101	102	103	104	105	106	107	108
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.178	0.181	0.181	0.178	0.184	0.175	0.173	0.184	0.167
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.153	0.173	0.173	0.170	0.175	0.170	0.173	0.175	0.175
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.178	0.181	0.181	0.178	0.184	0.175	0.173	0.184	0.167
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.186	0.186	0.186	0.184	0.189	0.181	0.178	0.189	0.173
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.178	0.181	0.181	0.178	0.184	0.175	0.173	0.184	0.167
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.178	0.170	0.170	0.164	0.173	0.164	0.162	0.173	0.156
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.175	0.184	0.184	0.181	0.186	0.175	0.181	0.186	0.175

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		109	110	111	112	113	114	115	116	117
29	NCG_N95_I16	0.019	0.018	0.020	0.020	0.020	0.016	0.020	0.020	0.020
30	NCU_N110_O211	0.018	0.020	0.019	0.019	0.019	0.020	0.019	0.019	0.019
31	NCW_N66_O280	0.018	0.020	0.018	0.018	0.018	0.020	0.018	0.019	0.018
32	NCY_N67_O282	0.019	0.021	0.018	0.018	0.018	0.022	0.018	0.019	0.018
33	NCZ_N110_O285	0.018	0.019	0.018	0.018	0.018	0.021	0.018	0.019	0.018
34	NDD_N101_O292	0.018	0.021	0.019	0.019	0.019	0.021	0.019	0.019	0.019
35	NDK_N94_O333	0.020	0.000	0.020	0.020	0.020	0.018	0.020	0.020	0.020
36	NDL_N96_O334	0.020	0.018	0.020	0.020	0.020	0.000	0.020	0.020	0.020
37	NEH_N112_BI22	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
38	NEM_N43_DW15	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
39	NEM_N43_AT53	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
40	NEW_N19_AD381	0.018	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020
41	NFN_N43_CG5	0.019	0.020	0.021	0.021	0.021	0.020	0.021	0.021	0.021
42	NFO_N127_CB26	0.019	0.019	0.020	0.020	0.020	0.019	0.020	0.020	0.020
43	NFZ_N122_BV095	0.020	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020
44	NGC_N129_CW5	0.020	0.019	0.019	0.019	0.019	0.018	0.019	0.020	0.019
45	NGE_N130_CW14	0.019	0.018	0.019	0.019	0.019	0.017	0.019	0.020	0.019
46	NGN_N19_DC5	0.018	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020
47	NGS_N136_DG10	0.020	0.021	0.019	0.019	0.019	0.021	0.019	0.020	0.019
48	NGV_N35_DW21	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.020	0.019
49	NIG_N22+N23_ID10	0.017	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
50	NK_N36_AD110	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
51	NRF_N7_NN11	0.019	0.020	0.016	0.016	0.016	0.020	0.016	0.018	0.016
52	NRG_N7_NN15	0.019	0.020	0.016	0.016	0.016	0.020	0.016	0.017	0.016
53	NRH_N7_NN16	0.020	0.020	0.016	0.016	0.016	0.020	0.016	0.017	0.016
54	NRI_N7_NN17	0.020	0.020	0.016	0.016	0.016	0.020	0.016	0.017	0.016
55	NRJ_N7_NN18	0.019	0.020	0.016	0.016	0.016	0.020	0.016	0.017	0.016
56	NRK_N7_NN20	0.020	0.020	0.015	0.015	0.015	0.020	0.015	0.017	0.015

[illegible]

		109	110	111	112	113	114	115	116	117
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.006	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.019	0.020	0.017	0.017	0.017	0.020	0.017	0.018	0.017
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.019	0.019	0.020	0.020	0.020	0.018	0.020	0.020	0.020
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.019	0.019	0.020	0.020	0.020	0.018	0.020	0.020	0.020
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.018	0.018	0.020	0.020	0.020	0.017	0.020	0.019	0.020
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.008	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.008	0.019	0.020	0.020	0.020	0.019	0.020	0.020	0.020
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.009	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.010	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.019	0.019	0.020	0.020	0.020	0.019	0.020	0.020	0.020
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.006	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.007	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301		0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.170		0.020	0.020	0.020	0.018	0.020	0.020	0.020
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.170	0.178		0.000	0.000	0.020	0.000	0.009	0.000
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.170	0.178	0.000		0.000	0.020	0.000	0.009	0.000

		109	110	111	112	113	114	115	116	117
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.170	0.178	0.000	0.000		0.020	0.000	0.009	0.000
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.170	0.145	0.178	0.178	0.178		0.020	0.020	0.020
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.170	0.178	0.000	0.000	0.000	0.178		0.009	0.000
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.173	0.186	0.030	0.030	0.030	0.178	0.030		0.009
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.170	0.178	0.000	0.000	0.000	0.178	0.000	0.030	
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314	0.162	0.195	0.063	0.063	0.063	0.181	0.063	0.077	0.063
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.181	0.189	0.055	0.055	0.055	0.170	0.055	0.044	0.055

		118	119
1	PC12	0.021	0.020
2	PC27	0.021	0.020
3	PC29	0.020	0.020
4	PC13	0.021	0.020
5	PC28	0.021	0.020
6	PC18	0.020	0.020
7	PC15	0.020	0.020
8	PC16	0.016	0.015
9	PC26	0.016	0.016
10	NA_N1_AG1	0.020	0.019
11	NAA_N45_AS38	0.020	0.020
12	NAB_N46_AS41	0.020	0.019
13	NAD_N93_AC10	0.021	0.021
14	NAM_N49_AD14	0.020	0.020
15	NAO_N22_AD328	0.019	0.020
16	NAQ_N5_AD352	0.017	0.017
17	NAW_N6_AD429	0.013	0.012
18	NAX_N24_AD452	0.020	0.020
19	NAZ_N6_AD457	0.014	0.015
20	NB_N16_AH8	0.020	0.020
21	NBC_N6_AD577	0.000	0.014
22	NBE_N46_AD583	0.021	0.021
23	NBM_N4_AD678	0.019	0.019
24	NBR_N14_AD746	0.020	0.020
25	NBT_N7_AD748	0.017	0.017
26	NBU_N15_AD753	0.019	0.020
27	NBW_N50_AD784	0.020	0.020
28	NCA_N20_AF78	0.020	0.020

		118	119
29	NCG_N95_I16	0.020	0.020
30	NCU_N110_O211	0.019	0.020
31	NCW_N66_O280	0.019	0.018
32	NCY_N67_O282	0.019	0.019
33	NCZ_N110_O285	0.019	0.019
34	NDD_N101_O292	0.019	0.020
35	NDK_N94_O333	0.021	0.020
36	NDL_N96_O334	0.020	0.020
37	NEH_N112_BI22	0.017	0.018
38	NEM_N43_DW15	0.021	0.021
39	NEM_N43_AT53	0.021	0.021
40	NEW_N19_AD381	0.019	0.021
41	NFN_N43_CG5	0.021	0.021
42	NFO_N127_CB26	0.020	0.020
43	NFZ_N122_BV095	0.020	0.020
44	NGC_N129_CW5	0.020	0.020
45	NGE_N130_CW14	0.019	0.020
46	NGN_N19_DC5	0.019	0.020
47	NGS_N136_DG10	0.019	0.020
48	NGV_N35_DW21	0.020	0.019
49	NIG_N22+N23_ID10	0.020	0.021
50	NK_N36_AD110	0.020	0.019
51	NRF_N7_NN11	0.017	0.017
52	NRG_N7_NN15	0.017	0.017
53	NRH_N7_NN16	0.018	0.017
54	NRI_N7_NN17	0.018	0.017
55	NRJ_N7_NN18	0.017	0.017
56	NRK_N7_NN20	0.017	0.016

		118	119
57	NRL_N7_NN21	0.017	0.016
58	NRM_N7_NN37	0.018	0.018
59	NRO_N7_NN38	0.017	0.017
60	NRP_N138_NN35	0.017	0.017
61	NRQ_N138_NN36	0.017	0.017
62	NRW_N144_OU21	0.020	0.020
63	NY_N37_AR64	0.020	0.019
64	T101209 Kwonkan MYG175 NHP	0.020	0.020
65	T112084 Synothele MYG127 NHD	0.019	0.019
66	T112949 Aname MYG227 NHG	0.019	0.019
67	T121597 Aname MYG250 NHQ	0.020	0.019
68	T122062 Aname MYG182 NGX	0.020	0.019
69	T96570 Aname MYG067 NHF	0.019	0.019
70	T98759 Aname MYG185 NHK	0.019	0.019
71	T98900 Aname MYG034 NHJ	0.014	0.000
72	JQ772136.1 <i>Aname</i> sp. 1 MGR-2012 voucher WAM:T95404	0.019	0.020
73	KJ744398.1 <i>Aname mellosa</i> voucher T101163	0.020	0.020
74	KJ744414.1 <i>Aname</i> sp. MYG178 voucher T102047	0.019	0.019
75	KJ744623.1 <i>Aname mellosa</i> voucher T105871	0.019	0.020
76	KJ744648.1 <i>Aname</i> sp. MYG373 voucher T107087	0.017	0.017
77	KJ744649.1 <i>Aname</i> sp. MYG373 voucher T107089	0.018	0.018
78	KJ744661.1 <i>Aname mellosa</i> voucher T107942	0.020	0.020
79	KJ744662.1 <i>Aname mellosa</i> voucher T107945	0.019	0.020
80	KJ744669.1 <i>Aname mellosa</i> voucher T107968	0.020	0.020
81	KJ744775.1 <i>Aname mellosa</i> voucher T113629	0.020	0.020
82	KJ744785.1 <i>Aname mellosa</i> voucher T113642	0.019	0.020
83	KJ744788.1 <i>Aname mellosa</i> voucher T113648	0.019	0.020
84	KJ744791.1 <i>Aname mellosa</i> voucher T113654	0.019	0.020

		118	119
85	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.019	0.020
86	KJ744901.1 <i>Aname</i> sp. MYG331 voucher T118789	0.017	0.018
87	KJ744902.1 <i>Aname</i> sp. MYG331 voucher T118791	0.017	0.018
88	KJ744909.1 <i>Aname</i> sp. MYG331 voucher T118805	0.017	0.017
89	KJ744910.1 <i>Aname</i> sp. MYG331 voucher T118811	0.017	0.018
90	KJ744911.1 <i>Aname</i> sp. MYG331 voucher T118812	0.017	0.018
91	KJ744914.1 <i>Aname</i> sp. MYG331 voucher T118818	0.017	0.018
92	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.019	0.020
93	KJ744963.1 <i>Kwonkan</i> sp. MYG337 voucher T120001	0.020	0.019
94	KJ744964.1 <i>Kwonkan</i> sp. MYG337 voucher T120003	0.020	0.019
95	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.020	0.019
96	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.020	0.020
97	KJ744982.1 <i>Aname mellosa</i> voucher T122207	0.020	0.020
98	KJ744987.1 <i>Aname mellosa</i> voucher T122215	0.020	0.020
99	KJ744990.1 <i>Aname mellosa</i> voucher T122219	0.020	0.020
100	KJ745117.1 <i>Aname</i> sp. MYG335 voucher T125329	0.020	0.020
101	KJ745134.1 <i>Aname mellosa</i> voucher T126250	0.020	0.020
102	KJ745143.1 <i>Aname mellosa</i> voucher T126259	0.020	0.020
103	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.019	0.020
104	KJ745153.1 <i>Aname mellosa</i> voucher T126271	0.020	0.020
105	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.019	0.020
106	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.019	0.020
107	KJ745160.1 <i>Aname mellosa</i> voucher T126280	0.020	0.020
108	KJ745168.1 <i>Aname mellosa</i> voucher T126296	0.019	0.020
109	KJ745170.1 <i>Aname mellosa</i> voucher T126301	0.019	0.020
110	KJ745210.1 <i>Kwonkan</i> sp. MYG343 voucher T57563	0.021	0.020
111	KJ745231.1 <i>Aname</i> sp. MYG351 voucher T74238	0.013	0.012
112	KJ745232.1 <i>Aname</i> sp. MYG351 voucher T74241	0.013	0.012

		118	119
113	KJ745233.1 <i>Aname</i> sp. MYG351 voucher T74247	0.013	0.012
114	KJ745281.1 <i>Kwonkan</i> sp. MYG361 voucher T78543	0.020	0.020
115	KJ745287.1 <i>Aname</i> sp. MYG351 voucher T82303	0.013	0.012
116	KJ745288.1 <i>Aname</i> sp. MYG351 voucher T82304	0.014	0.011
117	KJ745293.1 <i>Aname</i> sp. MYG351 voucher T82309	0.013	0.012
118	KJ745375.1 <i>Aname</i> sp. MYG034 voucher T93314		0.014
119	KJ745494.1 <i>Aname</i> sp. MYG034 voucher T98900	0.079	

		1	2	3	4	5	6	7	8	9
1	PC01		0.012	0.003	0.012	0.008	0.012	0.007	0.007	0.016
2	PC02	0.076		0.012	0.000	0.013	0.000	0.012	0.012	0.017
3	PC04	0.004	0.076		0.012	0.008	0.012	0.007	0.007	0.016
4	PC06	0.076	0.000	0.076		0.013	0.000	0.012	0.012	0.017
5	NN01	0.030	0.086	0.030	0.086		0.013	0.004	0.005	0.017
6	NN03	0.076	0.000	0.076	0.000	0.086		0.012	0.012	0.017
7	NN04	0.026	0.078	0.026	0.078	0.008	0.078		0.004	0.017
8	NN09	0.024	0.080	0.028	0.080	0.014	0.080	0.010		0.017
9	EF122605.2	0.160	0.184	0.160	0.184	0.166	0.184	0.166	0.168	
10	EF122607.2	0.160	0.184	0.160	0.184	0.166	0.184	0.166	0.168	0.000
11	EF122608.2	0.160	0.190	0.160	0.190	0.166	0.190	0.166	0.168	0.016
12	EF122612.2	0.158	0.186	0.158	0.186	0.164	0.186	0.164	0.166	0.004
13	EU381064.1	0.158	0.186	0.158	0.186	0.164	0.186	0.164	0.166	0.002
14	EU404114.1	0.160	0.182	0.160	0.182	0.164	0.182	0.164	0.168	0.030
15	HM567381.1	0.156	0.162	0.156	0.162	0.172	0.162	0.168	0.162	0.170
16	JF700146.1	0.168	0.184	0.164	0.184	0.182	0.184	0.182	0.184	0.160
17	JN018153.1	0.142	0.126	0.142	0.126	0.150	0.126	0.144	0.146	0.172
18	JN018154.1	0.156	0.154	0.160	0.154	0.162	0.154	0.154	0.152	0.172
19	JN018210.1	0.148	0.150	0.148	0.150	0.156	0.150	0.156	0.154	0.164
20	JN018211.1	0.156	0.160	0.160	0.160	0.154	0.160	0.158	0.152	0.194
21	KF997876.1	0.160	0.168	0.164	0.168	0.164	0.168	0.160	0.162	0.158
22	KT716037.1	0.158	0.140	0.158	0.140	0.162	0.140	0.154	0.152	0.168
23	KX648425.1	0.166	0.160	0.164	0.160	0.166	0.160	0.166	0.168	0.188
24	KX648429.1	0.166	0.160	0.164	0.160	0.166	0.160	0.166	0.168	0.188
25	KY982184.1	0.162	0.156	0.162	0.156	0.162	0.156	0.162	0.160	0.118
26	KY982185.1	0.160	0.178	0.160	0.178	0.166	0.178	0.166	0.168	0.026
27	KY982187.1	0.158	0.140	0.162	0.140	0.170	0.140	0.164	0.168	0.148

		1	2	3	4	5	6	7	8	9
28	KY982188.1	0.160	0.142	0.164	0.142	0.168	0.142	0.162	0.166	0.138
29	KY982192.1	0.172	0.182	0.172	0.182	0.182	0.182	0.180	0.178	0.126
30	KY982193.1	0.170	0.180	0.170	0.180	0.180	0.180	0.178	0.176	0.126
31	KY982194.1	0.162	0.170	0.162	0.170	0.168	0.170	0.166	0.164	0.122
32	KY982199.1	0.164	0.172	0.164	0.172	0.166	0.172	0.160	0.166	0.114
33	KY982273.1	0.162	0.152	0.162	0.152	0.174	0.152	0.170	0.168	0.166
34	MF422313.1	0.130	0.136	0.126	0.136	0.132	0.136	0.130	0.124	0.178
35	MF422319.1	0.156	0.138	0.156	0.138	0.160	0.138	0.152	0.146	0.166
36	MF422320.1	0.156	0.138	0.156	0.138	0.160	0.138	0.152	0.146	0.168
37	MF422321.1	0.152	0.134	0.152	0.134	0.156	0.134	0.148	0.146	0.164
38	MF422322.1	0.156	0.138	0.156	0.138	0.160	0.138	0.152	0.146	0.168
39	MF422326.1	0.144	0.150	0.144	0.150	0.160	0.150	0.156	0.146	0.152
40	MF422327.1	0.146	0.154	0.142	0.154	0.154	0.154	0.150	0.148	0.138
41	MF422328.1	0.146	0.156	0.146	0.156	0.166	0.156	0.162	0.156	0.144
42	MF422329.1	0.146	0.154	0.142	0.154	0.154	0.154	0.150	0.148	0.140
43	MF422330.1	0.146	0.154	0.142	0.154	0.154	0.154	0.150	0.148	0.138
44	MK479161.1	0.174	0.168	0.170	0.168	0.176	0.168	0.174	0.172	0.140
45	MK479165.1	0.172	0.180	0.172	0.180	0.168	0.180	0.170	0.166	0.128
46	MK479171.1	0.166	0.178	0.166	0.178	0.172	0.178	0.172	0.166	0.118
47	MK479180.1	0.166	0.162	0.170	0.162	0.172	0.162	0.166	0.168	0.122
48	MK479188.1	0.174	0.168	0.174	0.168	0.176	0.168	0.178	0.176	0.102
49	MK479196.1	0.162	0.156	0.158	0.156	0.166	0.156	0.164	0.166	0.120
50	MK479202.1	0.156	0.160	0.156	0.160	0.156	0.160	0.152	0.158	0.100
51	MK479204.1	0.152	0.160	0.156	0.160	0.162	0.160	0.156	0.154	0.130
52	MK479207.1	0.152	0.156	0.152	0.156	0.152	0.156	0.148	0.150	0.108
53	MK479210.1	0.162	0.184	0.162	0.184	0.166	0.184	0.166	0.170	0.032
54	NC 037222.1	0.162	0.184	0.162	0.184	0.166	0.184	0.166	0.170	0.032
55	JN018156.1	0.200	0.186	0.204	0.186	0.208	0.186	0.204	0.198	0.208

		1	2	3	4	5	6	7	8	9
56	KY295225.1	0.186	0.170	0.186	0.170	0.200	0.170	0.192	0.194	0.218
57	JN018163.1	0.196	0.196	0.196	0.196	0.206	0.196	0.198	0.198	0.198
58	HM418309.1	0.212	0.190	0.216	0.190	0.218	0.190	0.214	0.206	0.228
59	KF548118.1	0.186	0.182	0.186	0.182	0.200	0.182	0.196	0.192	0.186

		10	11	12	13	14	15	16	17	18
1	PC01	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.016	0.016
2	PC02	0.017	0.018	0.017	0.017	0.017	0.016	0.017	0.015	0.016
3	PC04	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.016	0.016
4	PC06	0.017	0.018	0.017	0.017	0.017	0.016	0.017	0.015	0.016
5	NN01	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.016	0.016
6	NN03	0.017	0.018	0.017	0.017	0.017	0.016	0.017	0.015	0.016
7	NN04	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.016	0.016
8	NN09	0.017	0.017	0.017	0.017	0.017	0.016	0.017	0.016	0.016
9	EF122605.2	0.000	0.006	0.003	0.002	0.008	0.017	0.016	0.017	0.017
10	EF122607.2		0.006	0.003	0.002	0.008	0.017	0.016	0.017	0.017
11	EF122608.2	0.016		0.006	0.006	0.008	0.017	0.017	0.017	0.017
12	EF122612.2	0.004	0.020		0.002	0.008	0.017	0.016	0.017	0.017
13	EU381064.1	0.002	0.018	0.002		0.008	0.017	0.016	0.017	0.017
14	EU404114.1	0.030	0.030	0.034	0.032		0.017	0.017	0.017	0.017
15	HM567381.1	0.170	0.172	0.166	0.168	0.172		0.015	0.016	0.018
16	JF700146.1	0.160	0.164	0.156	0.158	0.166	0.128		0.017	0.017
17	JN018153.1	0.172	0.176	0.172	0.174	0.180	0.158	0.174		0.016
18	JN018154.1	0.172	0.174	0.170	0.170	0.174	0.194	0.188	0.154	
19	JN018210.1	0.164	0.160	0.164	0.164	0.168	0.178	0.184	0.156	0.194
20	JN018211.1	0.194	0.198	0.196	0.196	0.202	0.186	0.202	0.088	0.162
21	KF997876.1	0.158	0.168	0.154	0.156	0.160	0.116	0.122	0.152	0.176
22	KT716037.1	0.168	0.172	0.166	0.166	0.168	0.142	0.182	0.168	0.174
23	KX648425.1	0.188	0.192	0.186	0.186	0.190	0.138	0.152	0.176	0.176
24	KX648429.1	0.188	0.192	0.186	0.186	0.190	0.138	0.152	0.176	0.176
25	KY982184.1	0.118	0.118	0.114	0.116	0.116	0.170	0.172	0.160	0.162
26	KY982185.1	0.026	0.026	0.030	0.028	0.008	0.170	0.166	0.176	0.168
27	KY982187.1	0.148	0.154	0.148	0.150	0.146	0.148	0.176	0.158	0.164

		10	11	12	13	14	15	16	17	18
28	KY982188.1	0.138	0.144	0.138	0.140	0.136	0.144	0.172	0.154	0.162
29	KY982192.1	0.126	0.132	0.126	0.124	0.138	0.154	0.168	0.176	0.154
30	KY982193.1	0.126	0.132	0.126	0.124	0.138	0.152	0.168	0.172	0.158
31	KY982194.1	0.122	0.128	0.118	0.120	0.134	0.138	0.162	0.166	0.156
32	KY982199.1	0.114	0.118	0.114	0.112	0.120	0.162	0.170	0.180	0.152
33	KY982273.1	0.166	0.168	0.170	0.168	0.162	0.160	0.176	0.164	0.196
34	MF422313.1	0.178	0.182	0.182	0.180	0.182	0.174	0.194	0.144	0.178
35	MF422319.1	0.166	0.170	0.164	0.164	0.170	0.136	0.186	0.162	0.168
36	MF422320.1	0.168	0.172	0.166	0.166	0.172	0.138	0.184	0.162	0.168
37	MF422321.1	0.164	0.168	0.162	0.162	0.168	0.134	0.182	0.158	0.168
38	MF422322.1	0.168	0.172	0.166	0.166	0.172	0.138	0.184	0.162	0.168
39	MF422326.1	0.152	0.160	0.150	0.150	0.152	0.146	0.186	0.156	0.182
40	MF422327.1	0.138	0.146	0.136	0.136	0.142	0.136	0.182	0.160	0.174
41	MF422328.1	0.144	0.152	0.142	0.142	0.146	0.128	0.182	0.154	0.178
42	MF422329.1	0.140	0.148	0.138	0.138	0.144	0.138	0.182	0.158	0.176
43	MF422330.1	0.138	0.146	0.136	0.136	0.142	0.136	0.182	0.160	0.174
44	MK479161.1	0.140	0.138	0.136	0.138	0.134	0.156	0.170	0.168	0.170
45	MK479165.1	0.128	0.128	0.128	0.126	0.130	0.160	0.178	0.178	0.164
46	MK479171.1	0.118	0.116	0.116	0.116	0.120	0.172	0.176	0.168	0.176
47	MK479180.1	0.122	0.124	0.120	0.120	0.118	0.148	0.156	0.158	0.146
48	MK479188.1	0.102	0.110	0.100	0.100	0.112	0.152	0.174	0.170	0.162
49	MK479196.1	0.120	0.122	0.120	0.122	0.126	0.170	0.176	0.158	0.166
50	MK479202.1	0.100	0.102	0.098	0.098	0.106	0.168	0.164	0.158	0.156
51	MK479204.1	0.130	0.128	0.126	0.128	0.138	0.160	0.166	0.160	0.150
52	MK479207.1	0.108	0.110	0.106	0.106	0.108	0.178	0.178	0.164	0.142
53	MK479210.1	0.032	0.032	0.036	0.034	0.002	0.170	0.168	0.178	0.176
54	NC 037222.1	0.032	0.032	0.036	0.034	0.002	0.170	0.168	0.178	0.176
55	JN018156.1	0.208	0.210	0.206	0.206	0.214	0.208	0.224	0.198	0.202

		10	11	12	13	14	15	16	17	18
56	KY295225.1	0.218	0.224	0.216	0.216	0.210	0.218	0.212	0.208	0.204
57	JN018163.1	0.198	0.208	0.196	0.196	0.198	0.218	0.228	0.214	0.204
58	HM418309.1	0.228	0.232	0.230	0.228	0.228	0.242	0.246	0.192	0.208
59	KF548118.1	0.186	0.186	0.188	0.188	0.192	0.206	0.216	0.204	0.208

		19	20	21	22	23	24	25	26	27
1	PC01	0.016	0.016	0.016	0.016	0.017	0.017	0.016	0.016	0.016
2	PC02	0.016	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.016
3	PC04	0.016	0.016	0.017	0.016	0.017	0.017	0.016	0.016	0.016
4	PC06	0.016	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.016
5	NN01	0.016	0.016	0.017	0.016	0.017	0.017	0.016	0.017	0.017
6	NN03	0.016	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.016
7	NN04	0.016	0.016	0.016	0.016	0.017	0.017	0.016	0.017	0.017
8	NN09	0.016	0.016	0.016	0.016	0.017	0.017	0.016	0.017	0.017
9	EF122605.2	0.017	0.018	0.016	0.017	0.017	0.017	0.014	0.007	0.016
10	EF122607.2	0.017	0.018	0.016	0.017	0.017	0.017	0.014	0.007	0.016
11	EF122608.2	0.016	0.018	0.017	0.017	0.018	0.018	0.014	0.007	0.016
12	EF122612.2	0.017	0.018	0.016	0.017	0.017	0.017	0.014	0.008	0.016
13	EU381064.1	0.017	0.018	0.016	0.017	0.017	0.017	0.014	0.007	0.016
14	EU404114.1	0.017	0.018	0.016	0.017	0.018	0.018	0.014	0.004	0.016
15	HM567381.1	0.017	0.017	0.014	0.016	0.015	0.015	0.017	0.017	0.016
16	JF700146.1	0.017	0.018	0.015	0.017	0.016	0.016	0.017	0.017	0.017
17	JN018153.1	0.016	0.013	0.016	0.017	0.017	0.017	0.016	0.017	0.016
18	JN018154.1	0.018	0.016	0.017	0.017	0.017	0.017	0.016	0.017	0.017
19	JN018210.1		0.017	0.017	0.016	0.018	0.018	0.017	0.017	0.017
20	JN018211.1	0.172		0.017	0.016	0.017	0.017	0.018	0.018	0.017
21	KF997876.1	0.182	0.166		0.017	0.015	0.015	0.016	0.016	0.016
22	KT716037.1	0.158	0.160	0.186		0.017	0.017	0.016	0.017	0.016
23	KX648425.1	0.202	0.174	0.136	0.182		0.000	0.017	0.017	0.017
24	KX648429.1	0.202	0.174	0.136	0.182	0.000		0.017	0.017	0.017
25	KY982184.1	0.166	0.192	0.156	0.160	0.178	0.178		0.014	0.014
26	KY982185.1	0.166	0.202	0.160	0.164	0.188	0.188	0.110		0.016
27	KY982187.1	0.180	0.186	0.152	0.152	0.180	0.180	0.116	0.146	

		19	20	21	22	23	24	25	26	27
28	KY982188.1	0.176	0.178	0.144	0.142	0.174	0.174	0.116	0.136	0.010
29	KY982192.1	0.178	0.186	0.160	0.162	0.180	0.180	0.118	0.134	0.118
30	KY982193.1	0.174	0.182	0.160	0.160	0.176	0.176	0.114	0.134	0.114
31	KY982194.1	0.164	0.192	0.154	0.152	0.174	0.174	0.112	0.132	0.098
32	KY982199.1	0.166	0.198	0.154	0.150	0.176	0.176	0.122	0.114	0.120
33	KY982273.1	0.194	0.182	0.170	0.178	0.182	0.182	0.160	0.160	0.150
34	MF422313.1	0.160	0.170	0.186	0.172	0.172	0.172	0.180	0.178	0.174
35	MF422319.1	0.164	0.150	0.186	0.018	0.180	0.180	0.166	0.166	0.154
36	MF422320.1	0.166	0.150	0.184	0.016	0.180	0.180	0.164	0.168	0.152
37	MF422321.1	0.162	0.154	0.182	0.012	0.178	0.178	0.160	0.164	0.148
38	MF422322.1	0.166	0.150	0.184	0.016	0.180	0.180	0.164	0.168	0.152
39	MF422326.1	0.160	0.166	0.174	0.076	0.180	0.180	0.160	0.148	0.162
40	MF422327.1	0.156	0.174	0.172	0.066	0.170	0.170	0.148	0.138	0.156
41	MF422328.1	0.158	0.178	0.172	0.074	0.178	0.178	0.158	0.142	0.162
42	MF422329.1	0.158	0.176	0.174	0.068	0.170	0.170	0.146	0.140	0.156
43	MF422330.1	0.156	0.174	0.172	0.066	0.170	0.170	0.148	0.138	0.156
44	MK479161.1	0.182	0.190	0.170	0.158	0.174	0.174	0.108	0.128	0.130
45	MK479165.1	0.178	0.182	0.182	0.154	0.174	0.174	0.126	0.130	0.126
46	MK479171.1	0.174	0.186	0.162	0.176	0.188	0.188	0.134	0.114	0.140
47	MK479180.1	0.172	0.178	0.144	0.136	0.164	0.164	0.098	0.116	0.116
48	MK479188.1	0.160	0.180	0.152	0.146	0.184	0.184	0.110	0.110	0.124
49	MK479196.1	0.164	0.184	0.166	0.160	0.182	0.182	0.104	0.122	0.122
50	MK479202.1	0.160	0.190	0.138	0.148	0.170	0.170	0.102	0.100	0.134
51	MK479204.1	0.168	0.172	0.156	0.146	0.180	0.180	0.122	0.136	0.124
52	MK479207.1	0.170	0.186	0.150	0.154	0.172	0.172	0.100	0.102	0.136
53	MK479210.1	0.170	0.200	0.162	0.166	0.188	0.188	0.118	0.010	0.148
54	NC 037222.1	0.170	0.200	0.162	0.166	0.188	0.188	0.118	0.010	0.148
55	JN018156.1	0.194	0.206	0.230	0.192	0.222	0.222	0.194	0.212	0.198

		19	20	21	22	23	24	25	26	27
56	KY295225.1	0.214	0.216	0.206	0.202	0.208	0.208	0.192	0.212	0.192
57	JN018163.1	0.220	0.218	0.226	0.208	0.206	0.206	0.202	0.194	0.214
58	HM418309.1	0.206	0.206	0.234	0.222	0.238	0.238	0.220	0.228	0.226
59	KF548118.1	0.174	0.206	0.212	0.188	0.226	0.226	0.202	0.190	0.204

		28	29	30	31	32	33	34	35	36
1	PC01	0.016	0.017	0.017	0.016	0.017	0.016	0.015	0.016	0.016
2	PC02	0.016	0.017	0.017	0.017	0.017	0.016	0.015	0.015	0.015
3	PC04	0.017	0.017	0.017	0.016	0.017	0.016	0.015	0.016	0.016
4	PC06	0.016	0.017	0.017	0.017	0.017	0.016	0.015	0.015	0.015
5	NN01	0.017	0.017	0.017	0.017	0.017	0.017	0.015	0.016	0.016
6	NN03	0.016	0.017	0.017	0.017	0.017	0.016	0.015	0.015	0.015
7	NN04	0.016	0.017	0.017	0.017	0.016	0.017	0.015	0.016	0.016
8	NN09	0.017	0.017	0.017	0.017	0.017	0.017	0.015	0.016	0.016
9	EF122605.2	0.015	0.015	0.015	0.015	0.014	0.017	0.017	0.017	0.017
10	EF122607.2	0.015	0.015	0.015	0.015	0.014	0.017	0.017	0.017	0.017
11	EF122608.2	0.016	0.015	0.015	0.015	0.014	0.017	0.017	0.017	0.017
12	EF122612.2	0.015	0.015	0.015	0.014	0.014	0.017	0.017	0.017	0.017
13	EU381064.1	0.016	0.015	0.015	0.015	0.014	0.017	0.017	0.017	0.017
14	EU404114.1	0.015	0.015	0.015	0.015	0.015	0.016	0.017	0.017	0.017
15	HM567381.1	0.016	0.016	0.016	0.015	0.016	0.016	0.017	0.015	0.015
16	JF700146.1	0.017	0.017	0.017	0.016	0.017	0.017	0.018	0.017	0.017
17	JN018153.1	0.016	0.017	0.017	0.017	0.017	0.017	0.016	0.016	0.016
18	JN018154.1	0.016	0.016	0.016	0.016	0.016	0.018	0.017	0.017	0.017
19	JN018210.1	0.017	0.017	0.017	0.017	0.017	0.018	0.016	0.017	0.017
20	JN018211.1	0.017	0.017	0.017	0.018	0.018	0.017	0.017	0.016	0.016
21	KF997876.1	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017	0.017
22	KT716037.1	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.006	0.006
23	KX648425.1	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
24	KX648429.1	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
25	KY982184.1	0.014	0.014	0.014	0.014	0.015	0.016	0.017	0.017	0.017
26	KY982185.1	0.015	0.015	0.015	0.015	0.014	0.016	0.017	0.017	0.017
27	KY982187.1	0.004	0.014	0.014	0.013	0.015	0.016	0.017	0.016	0.016

		28	29	30	31	32	33	34	35	36
28	KY982188.1		0.014	0.014	0.013	0.014	0.016	0.017	0.016	0.016
29	KY982192.1	0.116		0.003	0.009	0.010	0.016	0.017	0.017	0.017
30	KY982193.1	0.112	0.004		0.009	0.010	0.016	0.017	0.017	0.017
31	KY982194.1	0.098	0.046	0.042		0.010	0.016	0.017	0.016	0.016
32	KY982199.1	0.118	0.058	0.058	0.054		0.016	0.017	0.016	0.016
33	KY982273.1	0.152	0.150	0.148	0.156	0.160		0.018	0.017	0.017
34	MF422313.1	0.180	0.176	0.176	0.176	0.180	0.190		0.016	0.016
35	MF422319.1	0.144	0.166	0.164	0.152	0.158	0.182	0.162		0.003
36	MF422320.1	0.142	0.166	0.164	0.156	0.158	0.180	0.162	0.006	
37	MF422321.1	0.138	0.162	0.160	0.152	0.154	0.176	0.164	0.006	0.004
38	MF422322.1	0.142	0.166	0.164	0.156	0.158	0.180	0.162	0.006	0.000
39	MF422326.1	0.156	0.172	0.170	0.162	0.172	0.174	0.162	0.074	0.068
40	MF422327.1	0.146	0.166	0.164	0.158	0.162	0.176	0.160	0.064	0.062
41	MF422328.1	0.152	0.164	0.162	0.156	0.174	0.166	0.168	0.072	0.074
42	MF422329.1	0.146	0.168	0.166	0.160	0.164	0.176	0.160	0.066	0.064
43	MF422330.1	0.146	0.166	0.164	0.158	0.162	0.176	0.160	0.064	0.062
44	MK479161.1	0.126	0.114	0.114	0.114	0.114	0.158	0.164	0.162	0.160
45	MK479165.1	0.120	0.120	0.120	0.122	0.118	0.152	0.178	0.152	0.148
46	MK479171.1	0.136	0.130	0.130	0.130	0.124	0.154	0.166	0.176	0.174
47	MK479180.1	0.108	0.122	0.118	0.108	0.112	0.160	0.176	0.144	0.142
48	MK479188.1	0.118	0.108	0.108	0.100	0.114	0.176	0.182	0.144	0.144
49	MK479196.1	0.116	0.116	0.116	0.112	0.110	0.148	0.172	0.162	0.164
50	MK479202.1	0.128	0.120	0.120	0.110	0.104	0.180	0.170	0.150	0.152
51	MK479204.1	0.118	0.116	0.116	0.102	0.114	0.162	0.178	0.140	0.140
52	MK479207.1	0.134	0.124	0.124	0.122	0.106	0.164	0.184	0.152	0.150
53	MK479210.1	0.138	0.140	0.140	0.136	0.122	0.164	0.180	0.168	0.170
54	NC 037222.1	0.138	0.140	0.140	0.136	0.122	0.164	0.180	0.168	0.170
55	JN018156.1	0.202	0.220	0.216	0.202	0.220	0.232	0.206	0.188	0.190

		28	29	30	31	32	33	34	35	36
56	KY295225.1	0.198	0.198	0.198	0.198	0.194	0.216	0.212	0.210	0.210
57	JN018163.1	0.212	0.202	0.200	0.202	0.190	0.198	0.214	0.206	0.204
58	HM418309.1	0.224	0.228	0.224	0.222	0.230	0.220	0.204	0.218	0.220
59	KF548118.1	0.204	0.198	0.194	0.196	0.188	0.200	0.210	0.198	0.198

[illegible]

		37	38	39	40	41	42	43	44	45
28	KY982188.1	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.015	0.015
29	KY982192.1	0.016	0.017	0.017	0.017	0.017	0.017	0.017	0.014	0.015
30	KY982193.1	0.016	0.017	0.017	0.017	0.016	0.017	0.017	0.014	0.015
31	KY982194.1	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.014	0.015
32	KY982199.1	0.016	0.016	0.017	0.016	0.017	0.017	0.016	0.014	0.014
33	KY982273.1	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.016	0.016
34	MF422313.1	0.017	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
35	MF422319.1	0.003	0.003	0.012	0.011	0.012	0.011	0.011	0.016	0.016
36	MF422320.1	0.003	0.000	0.011	0.011	0.012	0.011	0.011	0.016	0.016
37	MF422321.1		0.003	0.012	0.010	0.011	0.011	0.010	0.016	0.016
38	MF422322.1	0.004		0.011	0.011	0.012	0.011	0.011	0.016	0.016
39	MF422326.1	0.072	0.068		0.010	0.009	0.010	0.010	0.016	0.016
40	MF422327.1	0.058	0.062	0.048		0.009	0.002	0.000	0.016	0.016
41	MF422328.1	0.070	0.074	0.042	0.038		0.009	0.009	0.016	0.016
42	MF422329.1	0.060	0.064	0.050	0.002	0.040		0.002	0.016	0.016
43	MF422330.1	0.058	0.062	0.048	0.000	0.038	0.002		0.016	0.016
44	MK479161.1	0.158	0.160	0.158	0.156	0.150	0.156	0.156		0.014
45	MK479165.1	0.150	0.148	0.158	0.150	0.152	0.152	0.150	0.112	
46	MK479171.1	0.172	0.174	0.174	0.170	0.178	0.172	0.170	0.122	0.140
47	MK479180.1	0.140	0.142	0.142	0.136	0.134	0.138	0.136	0.090	0.110
48	MK479188.1	0.142	0.144	0.146	0.138	0.142	0.140	0.138	0.116	0.102
49	MK479196.1	0.160	0.164	0.162	0.156	0.154	0.158	0.156	0.102	0.100
50	MK479202.1	0.148	0.152	0.146	0.150	0.152	0.152	0.150	0.124	0.134
51	MK479204.1	0.138	0.140	0.162	0.154	0.158	0.156	0.154	0.116	0.100
52	MK479207.1	0.146	0.150	0.142	0.148	0.150	0.150	0.148	0.126	0.124
53	MK479210.1	0.166	0.170	0.150	0.140	0.144	0.142	0.140	0.132	0.132
54	NC 037222.1	0.166	0.170	0.150	0.140	0.144	0.142	0.140	0.132	0.132
55	JN018156.1	0.186	0.190	0.218	0.204	0.206	0.206	0.204	0.206	0.220

		37	38	39	40	41	42	43	44	45
56	KY295225.1	0.206	0.210	0.218	0.214	0.212	0.214	0.214	0.194	0.216
57	JN018163.1	0.206	0.204	0.208	0.212	0.218	0.212	0.212	0.208	0.210
58	HM418309.1	0.220	0.220	0.224	0.232	0.228	0.230	0.232	0.228	0.236
59	KF548118.1	0.194	0.198	0.206	0.208	0.206	0.210	0.208	0.206	0.216

		46	47	48	49	50	51	52	53	54
28	KY982188.1	0.015	0.014	0.014	0.014	0.015	0.014	0.015	0.015	0.015
29	KY982192.1	0.015	0.015	0.014	0.014	0.015	0.014	0.015	0.016	0.016
30	KY982193.1	0.015	0.014	0.014	0.014	0.015	0.014	0.015	0.016	0.016
31	KY982194.1	0.015	0.014	0.013	0.014	0.014	0.014	0.015	0.015	0.015
32	KY982199.1	0.015	0.014	0.014	0.014	0.014	0.014	0.014	0.015	0.015
33	KY982273.1	0.016	0.016	0.017	0.016	0.017	0.016	0.017	0.017	0.017
34	MF422313.1	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
35	MF422319.1	0.017	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.017
36	MF422320.1	0.017	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.017
37	MF422321.1	0.017	0.016	0.016	0.016	0.016	0.015	0.016	0.017	0.017
38	MF422322.1	0.017	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.017
39	MF422326.1	0.017	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
40	MF422327.1	0.017	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016
41	MF422328.1	0.017	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
42	MF422329.1	0.017	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
43	MF422330.1	0.017	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016
44	MK479161.1	0.015	0.013	0.014	0.014	0.015	0.014	0.015	0.015	0.015
45	MK479165.1	0.016	0.014	0.014	0.013	0.015	0.013	0.015	0.015	0.015
46	MK479171.1		0.014	0.014	0.015	0.014	0.016	0.014	0.014	0.014
47	MK479180.1	0.116		0.014	0.014	0.014	0.013	0.015	0.014	0.014
48	MK479188.1	0.118	0.104		0.015	0.013	0.014	0.013	0.014	0.014
49	MK479196.1	0.136	0.110	0.124		0.014	0.012	0.015	0.015	0.015
50	MK479202.1	0.106	0.104	0.098	0.116		0.015	0.010	0.014	0.014
51	MK479204.1	0.142	0.094	0.108	0.074	0.134		0.015	0.016	0.016
52	MK479207.1	0.108	0.122	0.092	0.132	0.056	0.128		0.014	0.014
53	MK479210.1	0.118	0.116	0.114	0.128	0.108	0.140	0.110		0.000
54	NC 037222.1	0.118	0.116	0.114	0.128	0.108	0.140	0.110	0.000	
55	JN018156.1	0.216	0.196	0.204	0.216	0.186	0.206	0.194	0.216	0.216

		46	47	48	49	50	51	52	53	54
56	KY295225.1	0.210	0.182	0.196	0.204	0.184	0.200	0.186	0.212	0.212
57	JN018163.1	0.206	0.204	0.212	0.208	0.182	0.220	0.188	0.200	0.200
58	HM418309.1	0.228	0.232	0.228	0.220	0.226	0.230	0.236	0.230	0.230
59	KF548118.1	0.188	0.190	0.200	0.190	0.192	0.204	0.190	0.194	0.194

		1	2	3	4	5	6	7	8	9
1	PC03		0.012	0.012	0.014	0.015	0.015	0.014	0.014	0.015
2	PC05	0.104		0.012	0.011	0.014	0.015	0.015	0.014	0.014
3	PC08	0.101	0.093		0.012	0.014	0.014	0.014	0.014	0.014
4	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.128	0.085	0.103		0.014	0.014	0.014	0.014	0.014
5	KT446990. <i>Brachistosternus paposo</i>	0.158	0.148	0.131	0.134		0.009	0.013	0.014	0.014
6	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.151	0.149	0.126	0.133	0.053		0.012	0.015	0.014
7	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.136	0.154	0.126	0.138	0.108	0.104		0.014	0.015
8	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.143	0.138	0.129	0.148	0.146	0.154	0.143		0.012
9	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.159	0.128	0.139	0.136	0.143	0.146	0.156	0.098	
10	KT446986.1 <i>Brachistosternus negrei</i>	0.153	0.153	0.146	0.138	0.111	0.096	0.121	0.161	0.139
11	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.138	0.124	0.143	0.138	0.164	0.158	0.139	0.131	0.131
12	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.131	0.121	0.126	0.139	0.134	0.138	0.128	0.114	0.109
13	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.148	0.131	0.133	0.123	0.141	0.146	0.123	0.118	0.106
14	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.146	0.123	0.134	0.121	0.141	0.151	0.136	0.119	0.116
15	AY156581.1 <i>Pandinus dictator</i>	0.139	0.144	0.133	0.136	0.154	0.153	0.149	0.139	0.134
16	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.169	0.154	0.149	0.158	0.159	0.153	0.159	0.163	0.164
17	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.154	0.141	0.138	0.143	0.151	0.153	0.167	0.144	0.153
18	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.153	0.159	0.151	0.158	0.151	0.149	0.151	0.163	0.163
19	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.136	0.134	0.134	0.128	0.148	0.161	0.139	0.153	0.138
20	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.144	0.153	0.144	0.151	0.154	0.156	0.166	0.167	0.154
21	KT188365.1 <i>Scorpio palmatus</i>	0.143	0.151	0.143	0.153	0.164	0.176	0.163	0.156	0.164
22	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.143	0.154	0.136	0.148	0.141	0.154	0.141	0.164	0.166
23	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.171	0.159	0.161	0.159	0.144	0.163	0.149	0.167	0.167
24	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.154	0.163	0.149	0.163	0.156	0.158	0.154	0.169	0.161
25	KF997876.1 <i>Mesobuthus gibbosus</i>	0.201	0.199	0.191	0.192	0.194	0.194	0.191	0.189	0.187
26	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.189	0.179	0.191	0.194	0.199	0.197	0.197	0.184	0.186
27	JN018154.1 <i>Parabuthus laevifrons</i>	0.186	0.186	0.189	0.189	0.174	0.171	0.169	0.184	0.182
28	JN018153.1 <i>Lychas mucronatus</i>	0.192	0.186	0.194	0.197	0.189	0.184	0.176	0.201	0.189
29	MF422319.1 <i>Lychas tricarinatus</i>	0.182	0.186	0.192	0.201	0.194	0.186	0.194	0.211	0.189
30	MF422313.1 <i>Isometrus</i> sp.	0.174	0.191	0.189	0.196	0.202	0.202	0.187	0.202	0.209
31	KX648429.1 <i>Compsobuthus weneri</i>	0.192	0.187	0.191	0.192	0.197	0.187	0.189	0.211	0.197
32	EF122605.2 <i>Centruroides vittatus</i>	0.177	0.187	0.192	0.197	0.174	0.179	0.174	0.177	0.179
33	MK479161.1 <i>Centruroides arctimanus</i>	0.184	0.186	0.194	0.181	0.184	0.172	0.189	0.189	0.177
34	KY982184.1 <i>Centruroides schmidtii</i>	0.181	0.179	0.181	0.181	0.174	0.166	0.177	0.167	0.164
35	KY982273.1 <i>Zabius fuscus</i>	0.209	0.222	0.221	0.201	0.187	0.186	0.181	0.211	0.196

		1	2	3	4	5	6	7	8	9
36	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.146	0.143	0.153	0.141	0.159	0.153	0.153	0.186	0.164
37	HM418309.1 <i>lurus kinzelbachi</i> voucher VF-0846-1	0.164	0.161	0.176	0.151	0.172	0.149	0.153	0.191	0.172

		10	11	12	13	14	15	16	17	18
1	PC03	0.015	0.014	0.014	0.014	0.014	0.014	0.015	0.015	0.015
2	PC05	0.015	0.013	0.013	0.014	0.013	0.014	0.015	0.014	0.015
3	PC08	0.014	0.014	0.014	0.014	0.014	0.014	0.015	0.014	0.015
4	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.014	0.014	0.014	0.013	0.013	0.014	0.015	0.014	0.015
5	KT446990. <i>Brachistosternus paposo</i>	0.013	0.015	0.014	0.014	0.014	0.015	0.015	0.015	0.015
6	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.012	0.015	0.014	0.014	0.015	0.015	0.015	0.015	0.015
7	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.013	0.014	0.014	0.013	0.014	0.015	0.015	0.015	0.015
8	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.015	0.014	0.013	0.013	0.013	0.014	0.015	0.014	0.015
9	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.014	0.014	0.013	0.013	0.013	0.014	0.015	0.015	0.015
10	KT446986.1 <i>Brachistosternus negrei</i>		0.014	0.014	0.014	0.015	0.015	0.015	0.015	0.014
11	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.144		0.012	0.013	0.013	0.014	0.015	0.014	0.015
12	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.128	0.103		0.013	0.013	0.013	0.015	0.014	0.014
13	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.141	0.118	0.111		0.010	0.015	0.015	0.015	0.014
14	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.151	0.114	0.118	0.070		0.015	0.015	0.014	0.015
15	AY156581.1 <i>Pandinus dictator</i>	0.163	0.146	0.121	0.151	0.154		0.015	0.012	0.015
16	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.149	0.156	0.154	0.161	0.159	0.174		0.016	0.013
17	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.161	0.148	0.126	0.159	0.143	0.103	0.177		0.015
18	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.141	0.154	0.133	0.143	0.158	0.171	0.119	0.164	
19	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.131	0.143	0.141	0.126	0.131	0.148	0.156	0.153	0.163
20	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.159	0.163	0.139	0.151	0.159	0.126	0.167	0.128	0.169
21	KT188365.1 <i>Scorpio palmatus</i>	0.166	0.151	0.151	0.146	0.144	0.149	0.154	0.153	0.166
22	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.149	0.149	0.133	0.148	0.151	0.153	0.139	0.158	0.148
23	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.149	0.144	0.144	0.161	0.151	0.159	0.100	0.149	0.124
24	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.158	0.153	0.144	0.158	0.151	0.176	0.133	0.166	0.093
25	KF997876.1 <i>Mesobuthus gibbosus</i>	0.194	0.177	0.169	0.186	0.181	0.171	0.199	0.199	0.201
26	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.207	0.186	0.164	0.177	0.196	0.174	0.196	0.196	0.199
27	JN018154.1 <i>Parabuthus laevifrons</i>	0.187	0.176	0.164	0.187	0.197	0.189	0.184	0.194	0.177
28	JN018153.1 <i>Lychas mucronatus</i>	0.197	0.186	0.189	0.177	0.184	0.196	0.189	0.194	0.187
29	MF422319.1 <i>Lychas tricarinatus</i>	0.184	0.184	0.181	0.179	0.182	0.199	0.211	0.197	0.189
30	MF422313.1 <i>Isometrus</i> sp.	0.211	0.196	0.189	0.196	0.187	0.199	0.216	0.199	0.202
31	KX648429.1 <i>Compsobuthus weneri</i>	0.207	0.191	0.182	0.211	0.209	0.194	0.224	0.194	0.199
32	EF122605.2 <i>Centruroides vittatus</i>	0.187	0.176	0.153	0.179	0.182	0.167	0.179	0.176	0.182
33	MK479161.1 <i>Centruroides arctimanus</i>	0.201	0.182	0.169	0.191	0.184	0.177	0.201	0.176	0.186
34	KY982184.1 <i>Centruroides schmidtii</i>	0.181	0.164	0.172	0.176	0.174	0.167	0.181	0.158	0.174
35	KY982273.1 <i>Zabius fuscus</i>	0.199	0.196	0.182	0.191	0.204	0.194	0.202	0.196	0.184

		10	11	12	13	14	15	16	17	18
36	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.146	0.156	0.154	0.143	0.139	0.179	0.154	0.187	0.154
37	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.138	0.161	0.166	0.171	0.164	0.164	0.163	0.191	0.181

		19	20	21	22	23	24	25	26	27
1	PC03	0.014	0.014	0.014	0.014	0.015	0.015	0.016	0.016	0.016
2	PC05	0.014	0.015	0.015	0.015	0.015	0.015	0.016	0.016	0.016
3	PC08	0.014	0.014	0.014	0.014	0.015	0.015	0.016	0.016	0.016
4	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.014	0.015	0.015	0.014	0.015	0.015	0.016	0.016	0.016
5	KT446990. <i>Brachistosternus paposo</i>	0.014	0.015	0.015	0.014	0.014	0.015	0.016	0.016	0.015
6	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.015	0.015	0.016	0.015	0.015	0.015	0.016	0.016	0.015
7	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.014	0.015	0.015	0.014	0.015	0.015	0.016	0.016	0.015
8	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.015	0.015	0.015	0.015	0.015	0.015	0.016	0.016	0.016
9	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.014	0.015	0.015	0.015	0.015	0.015	0.016	0.016	0.016
10	KT446986.1 <i>Brachistosternus negrei</i>	0.014	0.015	0.015	0.015	0.015	0.015	0.016	0.017	0.016
11	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.014	0.015	0.015	0.015	0.014	0.015	0.016	0.016	0.016
12	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.014	0.014	0.015	0.014	0.014	0.014	0.015	0.015	0.015
13	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.014	0.015	0.014	0.014	0.015	0.015	0.016	0.016	0.016
14	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.014	0.015	0.014	0.015	0.015	0.015	0.016	0.016	0.016
15	AY156581.1 <i>Pandinus dictator</i>	0.014	0.014	0.015	0.015	0.015	0.016	0.015	0.015	0.016
16	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.015	0.015	0.015	0.014	0.012	0.014	0.016	0.016	0.016
17	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.015	0.014	0.015	0.015	0.015	0.015	0.016	0.016	0.016
18	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.015	0.015	0.015	0.014	0.013	0.012	0.016	0.016	0.016
19	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087		0.014	0.014	0.015	0.015	0.015	0.016	0.016	0.016
20	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.148		0.014	0.014	0.015	0.015	0.016	0.015	0.016
21	KT188365.1 <i>Scorpio palmatus</i>	0.133	0.138		0.015	0.015	0.015	0.016	0.016	0.016
22	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.153	0.148	0.163		0.014	0.015	0.016	0.016	0.016
23	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.167	0.164	0.161	0.129		0.014	0.017	0.017	0.016
24	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.158	0.171	0.166	0.149	0.139		0.016	0.016	0.016
25	KF997876.1 <i>Mesobuthus gibbosus</i>	0.194	0.187	0.204	0.184	0.207	0.194		0.013	0.015
26	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.192	0.172	0.197	0.191	0.207	0.201	0.124		0.015
27	JN018154.1 <i>Parabuthus laevifrons</i>	0.191	0.184	0.206	0.176	0.199	0.191	0.163	0.174	
28	JN018153.1 <i>Lychas mucronatus</i>	0.194	0.194	0.191	0.177	0.201	0.192	0.144	0.167	0.149
29	MF422319.1 <i>Lychas tricarinatus</i>	0.191	0.184	0.192	0.201	0.197	0.197	0.174	0.177	0.163
30	MF422313.1 <i>Isometrus</i> sp.	0.199	0.189	0.201	0.199	0.231	0.209	0.177	0.186	0.171
31	KX648429.1 <i>Compsobuthus weneri</i>	0.201	0.201	0.214	0.206	0.219	0.192	0.134	0.143	0.164
32	EF122605.2 <i>Centruroides vittatus</i>	0.171	0.164	0.172	0.174	0.181	0.176	0.151	0.151	0.156
33	MK479161.1 <i>Centruroides arctimanus</i>	0.186	0.191	0.194	0.186	0.212	0.174	0.154	0.153	0.158
34	KY982184.1 <i>Centruroides schmidtii</i>	0.187	0.186	0.194	0.177	0.199	0.186	0.141	0.163	0.149
35	KY982273.1 <i>Zabius fuscus</i>	0.194	0.214	0.202	0.199	0.207	0.214	0.166	0.177	0.184

		19	20	21	22	23	24	25	26	27
36	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.163	0.181	0.179	0.164	0.167	0.159	0.212	0.219	0.192
37	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.167	0.186	0.176	0.181	0.182	0.174	0.219	0.222	0.192

		28	29	30	31	32	33	34	35	36	37
1	PC03	0.016	0.016	0.015	0.016	0.016	0.016	0.016	0.017	0.014	0.015
2	PC05	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.014	0.015
3	PC08	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.015	0.016
4	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.014	0.015
5	KT446990. <i>Brachistosternus paposo</i>	0.016	0.016	0.016	0.016	0.015	0.016	0.015	0.016	0.015	0.015
6	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.016	0.016	0.016	0.016	0.016	0.015	0.015	0.016	0.015	0.015
7	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.016	0.015	0.015
8	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.016	0.017	0.016	0.017	0.016	0.016	0.015	0.017	0.016	0.016
9	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.016	0.016	0.017	0.016	0.016	0.016	0.015	0.016	0.015	0.015
10	KT446986.1 <i>Brachistosternus negrei</i>	0.016	0.016	0.017	0.017	0.016	0.016	0.016	0.016	0.014	0.014
11	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.016	0.016	0.016	0.016	0.016	0.016	0.015	0.016	0.015	0.015
12	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.016	0.016	0.016	0.016	0.015	0.015	0.015	0.016	0.015	0.015
13	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.016	0.016	0.016	0.017	0.016	0.016	0.016	0.016	0.014	0.015
14	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.016	0.016	0.016	0.017	0.016	0.016	0.015	0.016	0.014	0.015
15	AY156581.1 <i>Pandinus dictator</i>	0.016	0.016	0.016	0.016	0.015	0.016	0.015	0.016	0.016	0.015
16	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.016	0.017	0.017	0.017	0.016	0.016	0.016	0.016	0.015	0.015
17	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.016	0.016	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.016
18	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.016	0.016	0.016	0.016	0.016	0.016	0.015	0.016	0.015	0.016
19	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.016	0.015	0.015
20	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.017	0.016	0.016
21	KT188365.1 <i>Scorpio palmatus</i>	0.016	0.016	0.016	0.017	0.015	0.016	0.016	0.016	0.016	0.016
22	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.016	0.016	0.016	0.016	0.015	0.016	0.016	0.016	0.015	0.016
23	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.016	0.016	0.017	0.017	0.016	0.017	0.016	0.017	0.015	0.016
24	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.016	0.016	0.017	0.016	0.016	0.015	0.016	0.017	0.015	0.015
25	KF997876.1 <i>Mesobuthus gibbosus</i>	0.014	0.015	0.016	0.014	0.015	0.015	0.014	0.015	0.017	0.017
26	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.015	0.016	0.016	0.014	0.015	0.015	0.015	0.016	0.017	0.017
27	JN018154.1 <i>Parabuthus laevifrons</i>	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.016	0.016	0.016
28	JN018153.1 <i>Lychas mucronatus</i>		0.015	0.014	0.015	0.015	0.015	0.015	0.015	0.016	0.016
29	MF422319.1 <i>Lychas tricarinatus</i>	0.161		0.015	0.016	0.015	0.015	0.015	0.016	0.016	0.016
30	MF422313.1 <i>Isometrus</i> sp.	0.144	0.158		0.015	0.015	0.015	0.016	0.016	0.016	0.016
31	KX648429.1 <i>Compsobuthus weneri</i>	0.164	0.177	0.169		0.015	0.015	0.015	0.015	0.017	0.017
32	EF122605.2 <i>Centruroides vittatus</i>	0.163	0.161	0.163	0.174		0.014	0.013	0.015	0.016	0.016
33	MK479161.1 <i>Centruroides arctimanus</i>	0.158	0.156	0.156	0.159	0.133		0.012	0.015	0.016	0.017
34	KY982184.1 <i>Centruroides schmidtii</i>	0.158	0.161	0.177	0.166	0.116	0.101		0.015	0.016	0.016
35	KY982273.1 <i>Zabius fuscus</i>	0.161	0.181	0.186	0.172	0.159	0.161	0.154		0.017	0.017

		28	29	30	31	32	33	34	35	36	37
36	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.192	0.189	0.199	0.212	0.196	0.196	0.182	0.217		0.015
37	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.187	0.206	0.189	0.222	0.204	0.209	0.204	0.212	0.154	



Helix

Molecular Solutions

School of Animal Biology The University of Western Australia
Hackett Entrance No. 4 Hackett Drive Crawley WA 6009

PO Box 155
Leederville WA 6903

t: [08] 6488 4509

f: [08] 6488 1029

abn: 32 133 230 243

w: www.helixsolutions.com.au

5th December 2019

Penny Brooshooft
Senior Zoologist
Biota Environmental Sciences Pty Ltd
Level 1, 228 Carr Place
Leederville WA 6007

Via email

Re. Helix Job 601 - Report on the molecular systematics of the mygalomorph, and scorpion specimens from Winu.

Dear Penny,

Following is a summary of the results of the invertebrate molecular investigation we have completed for the Winu Fauna phase 2 survey. There were six species amongst the nine successfully sequenced invertebrate specimens, based on the current available molecular data. We detected four species amongst the six mygalomorph spider specimens, two of which have been recorded previously during phase one sampling. Amongst the three successfully sequenced scorpion specimens, two were placed in a single clade of the widely distributed species *Lychas annulatus* (family Buthidae). The remaining scorpion belonged to a separate widespread *Lychas* species, *Lychas adonis*. We were unable to obtain a good quality sequence from three specimens, and therefore the placement of these suspected buthid and urodacid scorpion specimens remain unresolved.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Zoë Hamilton, Dr. Terrie Finston and Yvette Hitchen
Helix Molecular Solutions



Background and Objective

The infraorder of Arachnida, Mygalomorphae, includes trapdoor spiders and their kin, and they are frequently identified as short-range endemics (SREs) (e.g. Harvey *et al.*, 2011; Castalanelli *et al.*, 2014). Identification of species has traditionally been performed using morphological techniques, however, only males can be used in identification, as both females and juveniles lack the diagnostic characters used in identification, and furthermore there is a large backlog of undescribed taxa. DNA barcoding with the use of COI mtDNA has become a rapid, objective method aiding mygalomorph species identifications and their distributions, and is recognised as providing important information that regulatory authorities can use to assess environmental impacts of large-scale developments (Harvey *et al.*, 2008; Environmental Protection Authority, 2009; Castalanelli *et al.*, 2014). Extensive molecular work has been conducted on the trap-door spider fauna of Western Australia (Helix, 2009a & b, 2010, 2011a - l, 2012a - i, 2013a & b, 2014a - d, 2015a - e, 2019a). The resulting dataset provides a molecular framework that can be used to provide regional context for localised sampling.

Six specimens of invertebrate fauna belonging to a single family of mygalomorph spiders (Araneae: Mygalomorphae: (Nemesiidae), and five scorpion specimens belonging to two families (Scorpionida: Buthidae & Urodacidae from the Winu survey area in the Little Sandy Desert were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI). The nine successful resulting molecular sequences were then assessed to determine the number of taxa present and compare these results to those specimens from Phase 1 sampling, as well as sequences publically available on GenBank, and those already in Helix's database for context.

Executive summary

- Six specimens of mygalomorph spiders from the Winu survey area were sequenced and assessed for variation at the COI mtDNA gene. The molecular data were then placed within an existing molecular taxonomic framework for each family, using COI mtDNA sequences from phase 1 sampling, GenBank, and mygalomorph COI sequences in the Helix database;
- Five scorpion (Scorpionida) specimens belonging to two families (Buthidae and Urodacidae) from the Winu survey area, in the Little Sandy Desert were sequenced and assessed for variation at the COI mtDNA gene. The resulting molecular data were then placed within an existing molecular taxonomic framework for each family, using COI mtDNA scorpions sequences from GenBank, and COI sequences in the Helix database;
- A single family (Nemesiidae) was amongst the six successfully sequenced spider specimens. Six haplotypes were amongst the six successfully sequenced mygalomorphae specimens;
- Two species of buthid (Buthidae) scorpions were recorded amongst the three specimens. These species were *Lychas annulatus* and *Lychas adonis*;
- One specimen of buthid scorpion was not successfully sequenced and therefore the placement of this suspected *Lychas* could not be ascertained;
- The single urodcaid specimen was not successfully sequenced and therefore the placement of this suspected *Urodacus* could not be ascertained.

Methods

Six mygalomorph spider specimens from four sampling locations (Table 1) were sequenced for variation at the cytochrome oxidase subunit I gene (COI) using primers LCOI & HCO2 (Folmer *et al.*, 1994). The resulting six mygalomorph sequences comprised six haplotypes (Table 2).

Five scorpion specimens from four sampling locations (Table 1) from two families (Buthidae and Urodacidae) were sequenced for variation at the cytochrome oxidase subunit I gene (COI) using primers LCOI & HCO2 (Folmer *et al.*, 1994). The three resulting successful scorpion sequences comprised three haplotypes (Table 2).

The two Winu specimens (mygalomorphs n=0, scorpions n=2) that were not successfully sequenced could not be assigned to known or unknown species. Sequence failure could be due to degradation of the DNA, primer mis-matches, or contamination by other DNA in the sample.

The sequences from the total nine successfully sequenced invertebrate individuals (COI) were edited using Geneious version 6.1.8 software (<https://www.geneious.com>) performed within MEGA version 5.05 (Tamura *et al.*, 2011) using the built-in alignment tool using CLUSTAL W (Thompson *et al.*, 1994) using default parameters. DNA nucleotide sequences were translated into protein sequences to ensure that the amplified sequences corresponded to the target mtDNA. The translated protein sequences were then checked for the presence of stop codons, to ensure that pseudogenes hadn't been amplified. Pseudogenes have a DNA sequence that is similar to the functional gene (e.g. COI) however, they do not code for a functioning protein despite the shared ancestry with the functional gene. The presence of pseudogenes can complicate molecular analyses, producing odd results. DNA sequences were translated into proteins with ExPASy using the invertebrate genetic code. All sequences analysed were of high quality with no evidence of heterogeneous peaks. All resulting sequences were 'BLAST'ed (Basic Local Alignment Search Tool) with the NCBI (National Centre for Biotechnology Information). This program compares DNA nucleotide sequences with a library of sequences and identifies sequences within the database that resemble the query sequences above a certain threshold. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotides different between sequences). To account for polymorphism within lineages, the net genetic diversity of Nei (1987) was calculated to give a 'corrected' distance between lineages.

For phylogenetic analysis, likelihood ratio tests using the Bayesian Information Criterion were calculated in MEGA 7.0 (Kumar *et al.*, 2016) to determine the best-fit model of evolution. The phylogenetic analyses were calculated in MEGA 7.0 (Kumar *et al.*, 2016) using maximum likelihood (ML) with 1000 bootstrap replicates, based on the genetic distances with the best-fit model of evolution calculated for each family. The tree was rooted using three outgroups, *Centruroides vittatus* (EU404114), *Mesobuthus martensii* (JF700146), and *Selenotholus* sp MYG381 (KJ744742) obtained from GenBank.

For the both the mygalomorph specimens (family Nemesiidae), and the scorpion specimens (family Buthidae) the best model of evolution was the General Time Reversible model with gamma distribution and invariant sites (GTR+G+I with the parameter for gamma distribution of 0.65 (Nemesiidae) and 0.76 (Buthidae).

Phylogenetic analysis were performed separately for each family, and included the representative haplotypes for the nine successfully sequenced specimens from the survey area, as well as a total of one-hundred and ninety seven reference specimens including all nemesiid mygalomorph specimens and all buthid specimens from phase 1 sampling, in addition to reference specimens obtained from both Helix and GenBank databases (Appendix 1).

Results

Mygalomorphae – family Nemesiidae

Phylogenetic Analyses

A 683 base-pair (bp) fragment of COI was isolated for all six nemesiid specimens from Winu.

Reference specimens and outgroups

The six mygalomorph specimens from the second phase of Winu fauna sampling (PP01 – PP06) were analysed along with a total of eighty-nine reference specimens from both the Helix database (n=54) and GenBank (n=35). These reference specimens also included representative lineages from the five species of nemesiid mygalomorph spiders recorded during phase 1 sampling (Helix 2019c). In addition to the thirty-five genbank sequences used for context, three specimens were also used during analyses as outgroups; these were *Centruroides vittatus* (EU404114), *Mesobuthus martensii* (JF700146), and *Selenotholus* sp MYG381 (KJ744742) all obtained from GenBank.

Based on phylogenetic analyses, the six nemesiid specimens from the second phase of sampling belong to four separate clades (Table 1, Figure 1). One specimen (PP01) shows affinity to the previously recorded species *Aname* sp. N148 (Figure 1, Table 1), recorded during phase one sampling. Three specimens (PP03, PP05, PP06) do not show affinity to any specimens available on GenBank, or in the Helix database. Another specimen (PP02) did not show affinity to any specimens available on GenBank or in the Helix database, and the placement of this specimen in relation to all other nemesiid specimens currently available for comparison is ambiguous, reflected by the low bootstrap support on the nodes (Figure 1). The remaining nemesiid specimen (PP04) showed affinity to the previously recorded species *Kwonkan* sp N15, recorded during phase one sampling.

Differentiation within and between lineages

Aname sp. N148 (PP01)

The PP01 specimen shows just 0.5 % sequence divergence from the nearest relative (NSA_N148_PC16, Table 3). There is 8.8 % divergence between PP01 and both NSB_N149_PC26 from the Helix database from the first phase of sampling for Winu and *Aname* sp. MYG351 (Genbank # KJ745288.1, WAM voucher # T82304) (Table 3, Figure 1). This species, *Aname* sp. N148 is represented by one other specimen in the Helix database, recorded during phase one sampling at Winu. Based on the limited molecular data of the specimens available for comparison, the species shows up to 1.0 % intraspecific sequence divergence.

Kwonkan sp. N151 (PP04)

The PP04 specimen from Winu shows 2.2 % sequence divergence from the nearest relative NSD_N151_PC13 (Figure 1, Table 3). The species, *Kwonkan* sp. N151 is represented by seven specimens in the Helix database recorded during phase one sampling. Based on the molecular data of the specimens available for comparison, the species shows up to 2.6 % intraspecific sequence divergence. The next closest relative, based on the molecular data available for comparison were NGE_N130_CW14 (Helix) and *Aname mellosa* (GenBank #KJ744982.1, WAM voucher T122207) both at 11.8 % sequence divergence (Table 3).

New species, *Aname* sp. N152 (PP03, PP05, PP06)

The three specimens from Winu show just 0.1 % sequence divergence from one another (Table 2). These specimens show 9.3 % sequence divergence from the nearest relatives (Table 3), *Aname* sp MYG331 (Genbank #'s KJ744911.1 & KJ744914.1, WAM voucher #'s T118812 & T118818). This suspected new species *Aname* sp. N152 is represented by just the three specimens collected during the second phase of sampling for Winu.

New species, *Aname* sp. N153 (PP02)

The final nemesiid specimen from Winu phase 2 sampling (PP02) shows 13.4 % sequence divergence from the nearest relative, *A. mellosa* (Genbank # KJ744982.1, WAM voucher T122207) (Figure 1, Table 3). This suspected new species, *Aname* sp. N153 is represented by just the single specimen collected during phase 2 sampling at Winu.

Scorpionida – family Buthidae

Over 40 scorpion species described in Australia are traditionally organized into four families: Buthidae, Bothriuridae, Urodacidae and Homuridae (Luna-Ramirez *et al.*, 2017). The Buthidae are the largest family of scorpions with 1053 species known under 92 genera (Rein, 2015). Few molecular investigations of phylogenetic relationships in the family Buthidae are available (Gantenbein *et al.*, 2000; 2003; Fet *et al.*, 2003; Gantenbein & Largiadèr, 2003; Mirshamsi *et al.*, 2010; Sousa *et al.*, 2010, 2011; Suranse *et al.*, 2017). Nevertheless, all these studies agree that morpho-taxonomy has limitations in differentiating and defining species boundaries, with findings that several currently recognized species are species groups comprising undescribed taxa. Morphological variability in buthids within taxa, along with morphological similarity between taxa, has led to taxonomic confusion and underscores the value of the inclusion of molecular data for species delineation in scorpions (Yamashita & Rhoads, 2013).

Previous sequencing by Helix of buthids from the Great Sandy Desert, approximately 40 km NW of the Winu collections (Helix, 2018, 2019a) and phase 1 at Winu (Helix, 2019b) revealed two closely related clades of Buthidae, which showed approximately 6 % sequence divergence (Helix, 2018; Helix, 2019b). Analyses of the Helix specimens performed by Dr Joel Huey (WA Museum) with his more extensive collection of sequences, not yet publically available, confirmed the placement of the Helix specimens in two distinct clades, which also contained specimens identified as *Lychas annulatus* by Lorenzo Prendini (American Museum of Natural History). This species is also recognised as *Hemilychas alexandrinus*, which according to the Atlas of Living Australia has a large distributional range across the arid zone of Australia. We refer to the two clades as *L. annulatus* clade A and *L. annulatus* clade B (Helix, 2018, Helix 2019b).

Reference specimens and outgroups

Three of the four specimens of buthid scorpions collected during the second phase of sampling at Winu were successfully sequenced (Table 1).

The three successfully sequenced specimens from the Winu study area comprised three haplotypes each of which was unique. These sequences were analysed along with one hundred reference scorpion specimens from GenBank (n= 83) and the Helix database (n= 17) from the family Buthidae. Five representative specimens from five additional scorpion families were used at outgroups in the analysis.

Phylogenetic Analyses

A 683 base-pair (bp) fragment of COI was isolated for the three successfully sequenced specimens. Amongst the three specimens, all had unique haplotypes. Phylogenetic analyses placed two of the haplotypes (PP07, PP11) in the previously detected *L. annulatus* clade B, along with specimens of *Lychas annulatus* from the first phase of sampling (Helix code PC) as well as specimens from the Helix databases collected from the Great Sandy Desert, (Helix code NN; Table 4).

While the two haplotypes from Winu phase 2 were both placed in *L. annulatus* clade B, haplotypes from phase 1 were placed in both clades A and B (Figure 2). *Lychas annulatus* clades A and B had a mean divergence of 6.8 % between them (Table 6).

The remaining Winu scorpion haplotype (PP08) belonged to another clade of *Lychas* scorpions (Figure 2). This specimen showed 9.4 % sequence divergence from the two *L. annulatus* specimens (PP07 & PP11), one of which (PP11) was collected at the same locality. This level of sequence divergence, along with the strongly supported phylogenetic differentiation clearly indicated a separate species of *Lychas* (Figure 2). For further resolution of this specimen, Dr. Erich Volschenk (Alacran Environmental Science) was consulted. This specimen has been included along with those buthid specimens in his collection, not yet publically available. Molecular analyses conducted by Dr Erich Volschenk indicate this specimen belongs to the

species *Lychas adonis*. The species has a widespread distribution across arid parts of Australia from Kalgoorlie to northern Victoria (Dr Erich Volschenck pers. comm., 2019).

Differentiation within and between lineages

Based on genetic distance of the specimens available for comparison, the *Lychas annulatus* clade B shows up to 2.3 % intraspecific sequence divergence (Table 4), with a mean divergence of 1.3 % (Table 5). The two clades (A & B) show up to 7.8 % sequence between them (Table 4). The pattern of differentiation amongst all specimens of *L. annulatus* does not follow an isolation by distance model. Rather, clade A shows no differentiation between specimens over 60 km (PC06 & NN03), whilst specimens less than 2.5 km distance apart (PP11 & PC02) show 7.2 % sequence divergence from one another. These phylogeographic patterns of differentiation suggest two distinct lineages, and these may well represent separate taxa, they will require further investigation for taxonomic resolution.

The closest relative to the phase 2 Winu *Lychas annulatus* clade B specimens (PP07 & PP11) was a specimen from the same clade collected (NN09) that showed 0.3 % sequence divergence (Table 4), followed by another specimen also collected from the Great Sandy Desert (NN04) with 1.0 % sequence divergence (Table 4). The closest relative obtained from GenBank specimen was an *Isometrus* sp. (MF422313.1) that showed 12.6 % sequence divergence (Table 4).

The closest relative to the *Lychas adonis* specimen (PP08), based on the publically available molecular data (GenBank) and those in the Helix database, was the *L. annulatus* specimen also collected from Winu (PP08) with 9.4% sequence divergence (Table 4).

Scorpionida – family Urodacidae

The Urodacidae is an Australian endemic family found across the continent, except on the south-eastern seaboard. It was first described by Koch (1977) and under the current classification includes two genera: *Urodacus* and the recently described troglobitic *Aops* (Volschenk & Prendini, 2008). The genus *Urodacus* is endemic in Australia; currently 22 valid species are recognised, although many more are known (Volschenk *et al.*, 2000; Volschenk *et al.*, 2010; Volschenk *et al.*, 2012; Luna-Ramirez *et al.*, 2017)

The single urodacid specimen collected during the second phase of sampling at Winu was not successfully sequenced and therefore taxonomic placement of this specimen could not be ascertained. Sequence failure could be due to degradation of the DNA, primer mismatches, or contamination by other DNA in the sample.

Conclusions

The mtDNA gene cytochrome oxidase 1 (COI) is widely considered to show suitable variation to distinguish species (Hebert *et al.*, 2003a), and the use of this gene can be extremely effective for 'DNA barcoding' in taxa where clear differentiation exists between intra and interspecific levels of divergence (e.g. Hebert *et al.*, 2004a; 2004b). In a comparison of COI sequences for over 13,000 pairs of taxa, Hebert *et al.* (2003b) found a mean of 11.1 % sequence divergence between distinct species. Nearly 80 % of these comparisons found that species pairs differed from one another by greater than 8 % sequence divergence. For mygalomorph spiders, the diversity of species in the Pilbara region of Western Australia was assessed to test the genetic relationships between and within species, and assess molecular results against morphotype designations comparing COI sequences for more than 1000 sequences from seven families, (Castalanelli *et al.*, 2014). The majority (92 %) of the morphotypes that had been previously recognised based on adult male morphology were recovered using sequence data, showing the utility of barcoding in mygalomorph spiders (Castalanelli *et al.*, 2014).

Despite its merits in barcoding however, a taxon by taxon approach, examining the amount of phylogenetic variation within and between taxa is the most widely accepted method of delineating species and their distributions, especially in areas where rapidly expanding mining operations outpace taxonomic treatment of unresolved taxa.

In summary, we detected a total of four species from a single family (Nemesiidae) among the six mygalomorph specimens and amongst the three successfully sequenced scorpion specimens we detected two species belonging to the Buthidae family. Two of the nemesiid mygalomorph species have been recorded previously, during phase one sampling, based on the sequences available for comparison, whilst four phase 2 nemesiid specimens appear to belong to two new species, neither of which have been detected previously, based on the molecular data available for comparison. The buthid scorpion species *Lychas annulatus* has been recorded previously, including during phase one sampling. The second buthid scorpion *Lychas adonis*, was not detected during phase one sampling but belongs to a widespread arid species.

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Table 1. . Invertebrate specimens used in the present study (Spiders n=6; Scorpions n=5), and the genetic lineage to which they belong. Coloured shading refers to colour-coding used to highlight species in Figures 1 & 2. Unshaded cells represent samples that failed to sequence.

Biota Sample ID	Helix ID	Order	Family	Genetic Lineage	Taxonomic ID
M20190924.WIN01P-01	PP01	Araneae	Nemesiidae	NSA	<i>Aname</i> sp. N148
M20190923.WIN02P-01	PP02	Araneae	Nemesiidae	NBF	<i>Aname</i> sp. N153
M20190923.WIN09P-02	PP03	Araneae	Nemesiidae	New species Lineage NSE	<i>Aname</i> sp. N152
M20190921.WINSRE12-01	PP04	Araneae	Nemesiidae	NSD	<i>Kwonkan</i> sp. N151
M20190923.WIN09P-01	PP05	Araneae	Nemesiidae	New species Lineage NSE	<i>Aname</i> sp. N152
M20190924.WIN09P-01	PP06	Araneae	Nemesiidae	New species Lineage NSE	<i>Aname</i> sp. N152
S20190919.WIN01P-01	PP07	Scorpionida	Buthidae	<i>Lychas annulatus</i> clade B	<i>Lychas annulatus</i> clade B
S20190919.WIN04P-02	PP08	Scorpionida	Buthidae	n/a	n/a
S20190922.WIN10P-01	PP09	Scorpionida	Urodacidae	n/a	n/a
S20190919.WIN05P-01	PP10	Scorpionida	Buthidae	<i>Lychas adonis</i>	<i>Lychas adonis</i>
S20190919.WIN04P-01	PP11	Scorpionida	Buthidae	<i>Lychas annulatus</i> clade B	<i>Lychas annulatus</i> clade B

Table 2. Genetic p-distance (below diagonal) and the associated standard error (above diagonal – blue text) between the six mygalomorph individuals, from the family Nemesiidae sequenced from the Winu survey area as shown in Figure 1. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

	PP01	PP02	PP03	PP04	PP05	PP06
PP01		0.013	0.012	0.014	0.012	0.012
PP02	0.142		0.013	0.014	0.013	0.013
PP03	0.111	0.142		0.014	0.001	0.001
PP04	0.164	0.157	0.151		0.014	0.014
PP05	0.113	0.142	0.001	0.152		0.000
PP06	0.113	0.142	0.001	0.152	0.000	

Table 3. Genetic p-distance (below diagonal) and the associated standard error (above diagonal – blue text) between the six Winu mygalomorph specimens, from the family Nemesiidae sequenced from the Winu survey area as shown in Figure 1. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 3 attached separately as a PDF document due to the size and detail.

Table 4. Genetic p-distance (below diagonal) and the associated standard error (above diagonal – blue text) between the three Winu scorpion specimens, from the family Buthidae sequenced from the Winu survey area as shown in Figure 2. Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance.

Table 4 attached separately as a PDF document due to the size and detail.

Table 5. Mean within group genetic distances for the two clades of *Lychas annulatus*.

	Mean genetic distance	s.e.
Clade A	0.017	0.002
Clade B	0.013	0.003

Table 6. Mean between group genetic distance between the two clades of *Lychas annulatus*.

	Mean genetic distance	s.e.
Clade A & Clade B	0.068	0.009

Figure 1 attached separately as a PDF document due to the size and detail.

Figure 1. Maximum likelihood analysis of mygalomorph COI mtDNA sequences, showing the placement of the Winu mygalomorphae specimens (sample prefix 'PP' for phase 2, 'PC' for phase 1) within the current taxonomic framework of the family Nemesiidae. Coloured boxes highlight the species to which the Winu specimen belongs. All sequences within 15 % sequence divergence are represented in the tree. 'N' numbers on tree refer to family species based on the 9.5 % species threshold tested in Castalanelli *et al.*, (2014). 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

Figure 2 attached separately as a PDF document due to the size and detail.

Figure 2. Maximum likelihood analysis of the three scorpion COI mtDNA haplotype sequences, showing the placement of the Winu buthids (sample prefix 'PP' for phase 2, 'PC' for phase 1) within the current taxonomic framework of the family Buthidae. Coloured box highlight the species to which the Winu specimens belong. All sequences within 15 % sequence divergence are represented in the tree. 'T' numbers refer to WA Museum registration code. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Bootstrap values <60 are not shown. Scale indicates inferred evolutionary distance (substitutions/site).

Appendix 1. Invertebrate reference specimens utilized during analysis in the present study, the source of the data, and the genetic lineage to which they belong.

Appendix 1 attached separately as a PDF document due to the size and detail.

Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
NA_N1_AG1	n/a	NA	N1	n/a	Helix database	Nemesiidae
NAI_N8_AD1	n/a	NAI	N8	n/a	Helix database	Nemesiidae
NAW_N6_AD429	n/a	NAW	N6	n/a	Helix database	Nemesiidae
NAZ_N6_AD457	n/a	NAZ	N6	n/a	Helix database	Nemesiidae
NBC_N6_AD577	n/a	NBC	N6	n/a	Helix database	Nemesiidae
NBE_N46_AD583	n/a	NBE	N46	n/a	Helix database	Nemesiidae
NBF_N11_AD592	n/a	NBF	N11	n/a	Helix database	Nemesiidae
NBR_N14_AD746	n/a	NBR	N14	n/a	Helix database	Nemesiidae
NBT_N7_AD748	n/a	NBT	N7	n/a	Helix database	Nemesiidae
NBU_N15_AD753	n/a	NBU	N15	n/a	Helix database	Nemesiidae
NBW_N50_AD784	n/a	NBW	N50	n/a	Helix database	Nemesiidae
NBY_N13_AF26b	n/a	NBY	N13	n/a	Helix database	Nemesiidae
NCU_N110_O211	n/a	NCU	N110	n/a	Helix database	Nemesiidae
NCW_N66_O280	n/a	NCW	N66	n/a	Helix database	Nemesiidae
NCY_N67_O282	n/a	NCY	N67	n/a	Helix database	Nemesiidae
NCZ_N110_O285	n/a	NCZ	N110	n/a	Helix database	Nemesiidae
NDC_N84_O288	n/a	NDC	N84	n/a	Helix database	Nemesiidae
NDD_N101_O292	n/a	NDD	N101	n/a	Helix database	Nemesiidae
NDG_N78_O304	n/a	NDG	N78	n/a	Helix database	Nemesiidae
NDK_N94_O333	n/a	NDK	N94	n/a	Helix database	Nemesiidae
NDL_N96_O334	n/a	NDL	N96	n/a	Helix database	Nemesiidae
NEH_N112_BI22	n/a	NEH	N112	n/a	Helix database	Nemesiidae
NEM_N43_DW15	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEM_N43_AT53	n/a	NEM	N43	n/a	Helix database	Nemesiidae
NEN_N115_AD594	n/a	NEN	N115	n/a	Helix database	Nemesiidae
NFN_N43_CG5	n/a	NFN	N43	n/a	Helix database	Nemesiidae
NFZ_N122_BV095	n/a	NFZ	N122	n/a	Helix database	Nemesiidae
NGE_N130_CW14	n/a	NGE	N130	n/a	Helix database	Nemesiidae

Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
NGS_N136_DG10	n/a	NGS	N136	n/a	Helix database	Nemesiidae
NGQ_N134_DG3	n/a	NGQ	N134	n/a	Helix database	Nemesiidae
NRC_N150_PC15	n/a	NRC	N150	n/a	Helix database	Nemesiidae
NRF_N7_NN11	n/a	NRF	N7	n/a	Helix database	Nemesiidae
NRG_N7_NN15	n/a	NRG	N7	n/a	Helix database	Nemesiidae
NRH_N7_NN16	n/a	NRH	N7	n/a	Helix database	Nemesiidae
NRI_N7_NN17	n/a	NRI	N7	n/a	Helix database	Nemesiidae
NRJ_N7_NN18	n/a	NRJ	N7	n/a	Helix database	Nemesiidae
NRK_N7_NN20	n/a	NRK	N7	n/a	Helix database	Nemesiidae
NRL_N7_NN21	n/a	NRL	N7	n/a	Helix database	Nemesiidae
NRM_N7_NN37	n/a	NRM	N7	n/a	Helix database	Nemesiidae
NRO_N7_NN38	n/a	NRO	N7	n/a	Helix database	Nemesiidae
NRP_N138_NN35	n/a	NRP	N138	n/a	Helix database	Nemesiidae
NRQ_N138_NN36	n/a	NRQ	N138	n/a	Helix database	Nemesiidae
NRZ_N147_PC18	n/a	NRZ	N147	n/a	Helix database	Nemesiidae
NSA_N148_PC16	n/a	NSA	N148	n/a	Helix database	Nemesiidae
NSB_N149_PC26	n/a	NSB	N149	n/a	Helix database	Nemesiidae
NSD_N151_PC13	n/a	NSD	N151	n/a	Helix database	Nemesiidae
NY_N37_AR64	n/a	NY	N37	n/a	Helix database	Nemesiidae
T101209	n/a	<i>Kwonkan</i>	MYG175	T101209	Helix database	Nemesiidae
T108978	n/a	<i>Aname</i>	MYG214	T108978	Helix database	Nemesiidae
T112084	n/a	<i>Synothele</i>	MYG127	T112084	Helix database	Nemesiidae
T112949	n/a	<i>Aname</i>	MYG227	T112949	Helix database	Nemesiidae
T96570	n/a	<i>Aname</i>	MYG067	T96570	Helix database	Nemesiidae
T98767	n/a	<i>Aname</i>	MYG102	T98767	Helix database	Nemesiidae
T98900	n/a	<i>Aname</i>	MYG034	T98900	Helix database	Nemesiidae
n/a	JQ772139	<i>Aname</i>	sp	T98892	GenBank	Nemesiidae
n/a	KJ744505	<i>Aname</i>	<i>melloso</i>	T103199	GenBank	Nemesiidae

Helix ID	Bank accession Nui	Genus	Species	Voucher	Source	Family
n/a	KJ744623	<i>Aname</i>	<i>mellosa</i>	T105871	GenBank	Nemesiidae
n/a	KJ744648	<i>Aname</i>	sp	T107087	GenBank	Nemesiidae
n/a	KJ744649	<i>Aname</i>	sp	T107089	GenBank	Nemesiidae
n/a	KJ744677	<i>Aname</i>	<i>mellosa</i>	T107987	GenBank	Nemesiidae
n/a	KJ744775	<i>Aname</i>	<i>mellosa</i>	T113629	GenBank	Nemesiidae
n/a	KJ744785	<i>Aname</i>	<i>mellosa</i>	T113642	GenBank	Nemesiidae
n/a	KJ744788	<i>Aname</i>	<i>mellosa</i>	T113648	GenBank	Nemesiidae
n/a	KJ744791	<i>Aname</i>	<i>mellosa</i>	T113654	GenBank	Nemesiidae
n/a	KJ744833	<i>Kwonkan</i>	sp	T114812	GenBank	Nemesiidae
n/a	KJ744901	<i>Aname</i>	sp	T118789	GenBank	Nemesiidae
n/a	KJ744902	<i>Aname</i>	sp	T118791	GenBank	Nemesiidae
n/a	KJ744909	<i>Aname</i>	sp	T118805	GenBank	Nemesiidae
n/a	KJ744910	<i>Aname</i>	sp	T118811	GenBank	Nemesiidae
n/a	KJ744911	<i>Aname</i>	sp	T118812	GenBank	Nemesiidae
n/a	KJ744914	<i>Aname</i>	sp	T118818	GenBank	Nemesiidae
n/a	KJ744982	<i>Aname</i>	<i>mellosa</i>	T122207	GenBank	Nemesiidae
n/a	KJ744987	<i>Aname</i>	<i>mellosa</i>	T122215	GenBank	Nemesiidae
n/a	KJ744989	<i>Aname</i>	<i>mellosa</i>	T122218	GenBank	Nemesiidae
n/a	KJ744990	<i>Aname</i>	<i>mellosa</i>	T122219	GenBank	Nemesiidae
n/a	KJ744992	<i>Aname</i>	<i>mellosa</i>	T122222	GenBank	Nemesiidae
n/a	KJ745155	<i>Aname</i>	<i>mellosa</i>	T126273	GenBank	Nemesiidae
n/a	KJ745231	<i>Aname</i>	sp	T74238	GenBank	Nemesiidae
n/a	KJ745232	<i>Aname</i>	sp	T74241	GenBank	Nemesiidae
n/a	KJ745233	<i>Aname</i>	sp	T74247	GenBank	Nemesiidae
n/a	KJ745281	<i>Kwonkan</i>	sp	T78543	GenBank	Nemesiidae
n/a	KJ745287	<i>Aname</i>	sp	T82303	GenBank	Nemesiidae
n/a	KJ745288	<i>Aname</i>	sp	T82304	GenBank	Nemesiidae
n/a	KJ745293	<i>Aname</i>	sp	T82309	GenBank	Nemesiidae

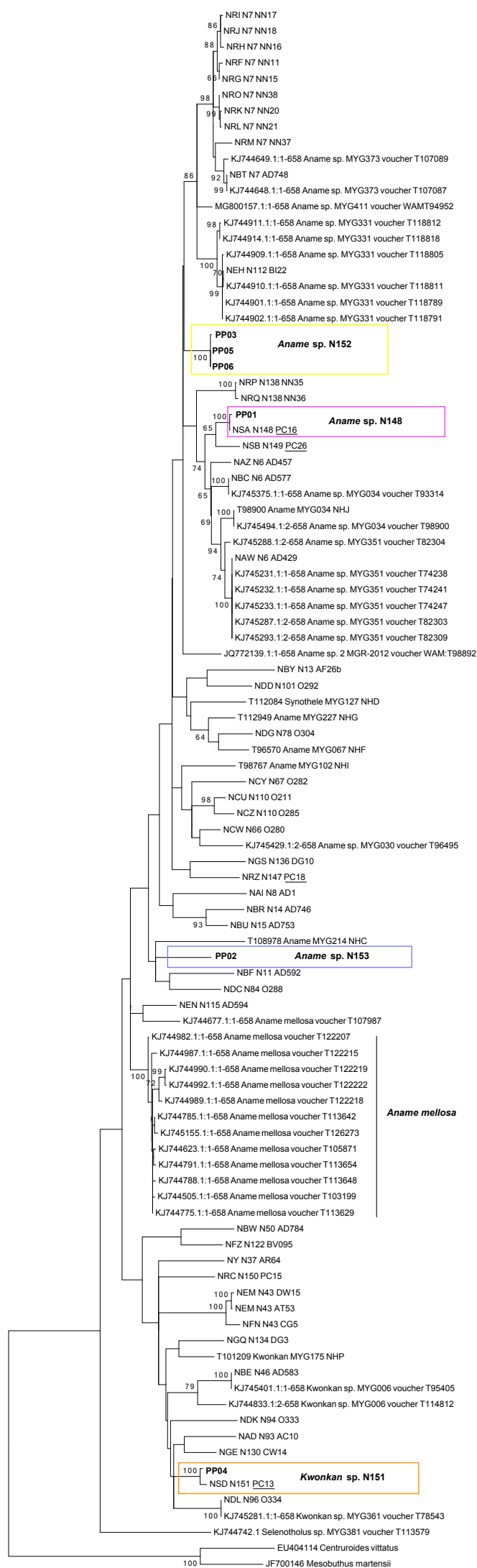
Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
n/a	KJ745375	<i>Aname</i>	sp	T93314	GenBank	Nemesiidae
n/a	KJ745401	<i>Kwonkan</i>	sp	T95405	GenBank	Nemesiidae
n/a	KJ745429	<i>Aname</i>	sp	T96495	GenBank	Nemesiidae
n/a	KJ745494	<i>Aname</i>	sp	T98900	GenBank	Nemesiidae
n/a	MG800157	<i>Aname</i>	sp	T94952	GenBank	Nemesiidae
n/a	EU404114	<i>Centruroides</i>	<i>vittatus</i>	n/a	GenBank	Buthidae
n/a	JF700146	<i>Mesobuthus</i>	<i>martensii</i>	n/a	GenBank	Buthidae
n/a	KJ7447421	<i>Selenotholus</i>	sp	T113579	GenBank	Theraphosidae
PC01	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
PC02	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
PC03	n/a	<i>Urodacus</i>	<i>varians</i>	n/a	Helix database	Urodacidae
PC04	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
PC05	n/a	<i>Urodacus</i>	sp. Telfer	n/a	Helix database	Urodacidae
PC06	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
PC07	n/a	<i>Urodacus</i>	<i>yaschenkoki</i>	n/a	Helix database	Urodacidae
PC08	n/a	<i>Urodacus</i>	<i>yaschenkoki</i>	n/a	Helix database	Urodacidae
NN01	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN03	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN04	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN05	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN06	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN07	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN08	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN09	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
NN10	n/a	<i>Lychas</i>	<i>annulatus</i>	n/a	Helix database	Buthidae
EF122605.2	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
KY295225.1	n/a	<i>Urodacus</i>	<i>planimanus</i>	WAM T129654	GenBank	Urodacidae
KT446990.	n/a	<i>Brachistosternus</i>	<i>paposo</i>		GenBank	Bothriuridae

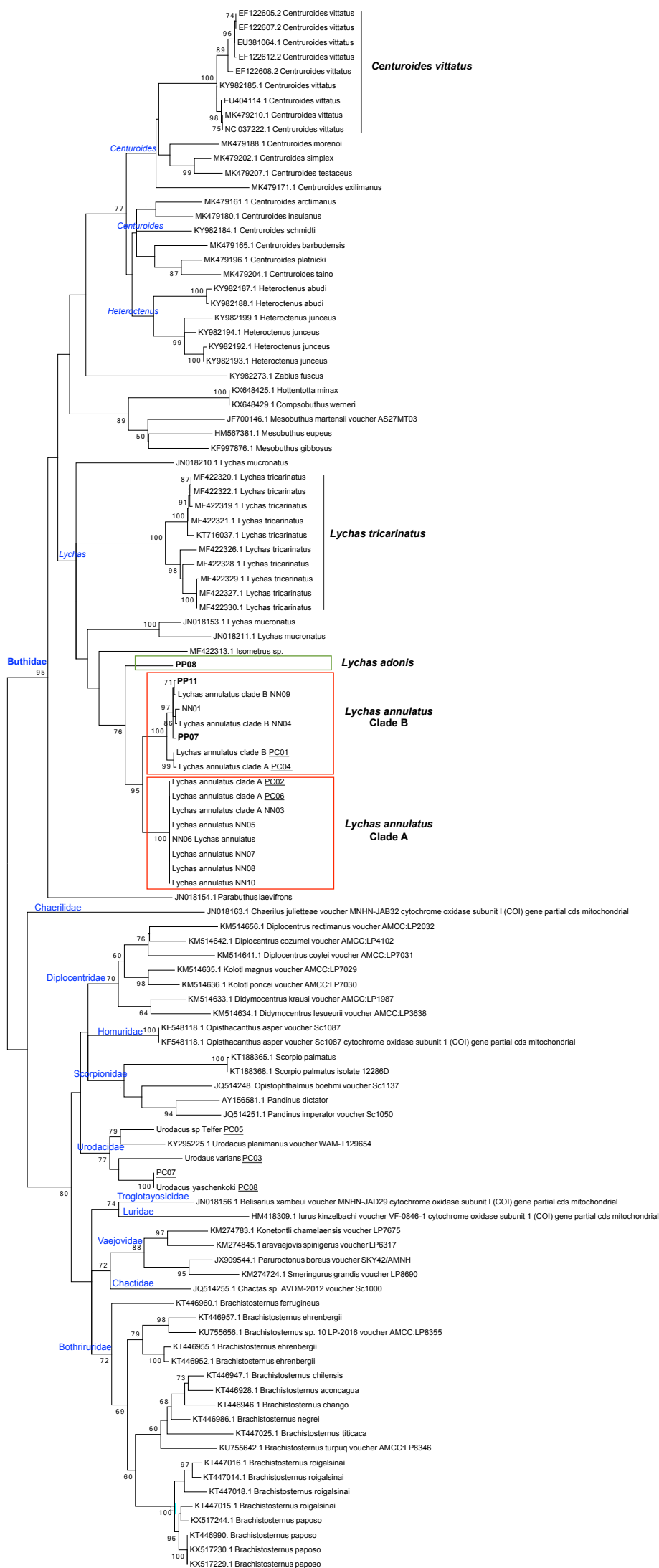
Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
KT447018.1	n/a	<i>Brachistosternus</i>	<i>roigalsinai</i>		GenBank	Bothriuridae
KT446957.1	n/a	<i>Brachistosternus</i>	<i>ehrenbergii</i>		GenBank	Bothriuridae
KM514656.1	n/a	<i>Diplocentrus</i>	<i>rectimanus</i>	AMCC LP2032	GenBank	Diplocentridae
KM514633.1	n/a	<i>Didymocentrus</i>	<i>krausi</i>	AMCC LP1987	GenBank	Diplocentridae
KM514635.1	n/a	<i>Kolotl</i>	<i>magnus</i>	AMCC LP7029	GenBank	Diplocentridae
KX517230.1	n/a	<i>Brachistosternus</i>	<i>paposo</i>		GenBank	Bothriuridae
KX517229.1	n/a	<i>Brachistosternus</i>	<i>paposo</i>		GenBank	Bothriuridae
KT446947.1	n/a	<i>Brachistosternus</i>	<i>chilensis</i>		GenBank	Bothriuridae
KT446928.1	n/a	<i>Brachistosternus</i>	<i>aconcagua</i>		GenBank	Bothriuridae
KM514636.1	n/a	<i>Kolotl</i>	<i>poncei</i>	AMCC LP7030	GenBank	Diplocentridae
AY156581.1	n/a	<i>Pandinus</i>	<i>dictator</i>		GenBank	Scorpionidae
KM514642.1	n/a	<i>Diplocentrus</i>	<i>cozumel</i>	AMCC LP4102	GenBank	Diplocentridae
KT447015.1	n/a	<i>Brachistosternus</i>	<i>roigalsinai</i>		GenBank	Bothriuridae
KT446955.1	n/a	<i>Brachistosternus</i>	<i>ehrenbergii</i>		GenBank	Bothriuridae
KT446946.1	n/a	<i>Brachistosternus</i>	<i>chango</i>		GenBank	Bothriuridae
KM274783.1	n/a	<i>Konetontli</i>	<i>chamelaensis</i>	LP7675	GenBank	Vaejovidae
KU755656.1	n/a	<i>Brachistosternus</i>	<i>sp.</i>	AMCC LP8355	GenBank	Bothriuridae
JQ514251.1	n/a	<i>Pandinus</i>	<i>imperator</i>	Sc1050	GenBank	Scorpionidae
KM514641.1	n/a	<i>Diplocentrus</i>	<i>coylei</i>	AMCC LP7031	GenBank	Diplocentridae
KX517244.1	n/a	<i>Brachistosternus</i>	<i>paposo</i>		GenBank	Bothriuridae
KU755642.1	n/a	<i>Brachistosternus</i>	<i>turpuq</i>	AMCC LP8346	GenBank	Bothriuridae
KT447016.1	n/a	<i>Brachistosternus</i>	<i>roigalsinai</i>		GenBank	Bothriuridae
KT446986.1	n/a	<i>Brachistosternus</i>	<i>negrei</i>		GenBank	Bothriuridae
KT446952.1	n/a	<i>Brachistosternus</i>	<i>ehrenbergii</i>		GenBank	Bothriuridae
JX909544.1	n/a	<i>Paruroctonus</i>	<i>boreus</i>	SKY42/AMNH	GenBank	Vaejovidae
KT446960.1	n/a	<i>Brachistosternus</i>	<i>ferrugineus</i>		GenBank	Bothriuridae
KM514634.1	n/a	<i>Didymocentrus</i>	<i>lesueurii</i>	AMCC LP3638	GenBank	Diplocentridae
KF548118.1	n/a	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae

Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
KT447025.1	n/a	<i>Brachistosternus</i>	<i>titicaca</i>		GenBank	Bothriuridae
KT447014.1	n/a	<i>Brachistosternus</i>	<i>roigalsinai</i>		GenBank	Bothriuridae
KT188365.1	n/a	<i>Scorpio</i>	<i>palmatus</i>		GenBank	Scorpionidae
JQ514255.1	n/a	<i>Chactas</i>	sp.	voucher	GenBank	Chactidae
JQ514248.	n/a	<i>Opisthophthalmus</i>	<i>boehmi</i>	Sc1137	GenBank	Homuridae
KM274845.1	n/a	<i>Paravaejovis</i>	<i>spinigerus</i>	LP6317	GenBank	Vaejovidae
KM274724.1	n/a	<i>Smeringurus</i>	<i>grandis</i>	LP8690	GenBank	Vaejovidae
KT188368.1	n/a	<i>Scorpio</i>	<i>palmatus</i>	12286D	GenBank	Scorpionidae
EF122607.2	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
EF122608.2	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
EF122612.2	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
EU381064.1	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
EU404114.1	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
HM567381.1	n/a	<i>Mesobuthus</i>	<i>eupeus</i>		GenBank	Buthidae
JF700146.1	n/a	<i>Mesobuthus</i>	<i>martensii</i>	AS27MT03	GenBank	Buthidae
JN018153.1	n/a	<i>Lychas</i>	<i>mucronatus</i>		GenBank	Buthidae
JN018154.1	n/a	<i>Parabuthus</i>	<i>laevifrons</i>		GenBank	Buthidae
JN018210.1	n/a	<i>Lychas</i>	<i>mucronatus</i>		GenBank	Buthidae
JN018211.1	n/a	<i>Lychas</i>	<i>mucronatus</i>		GenBank	Buthidae
KF997876.1	n/a	<i>Mesobuthus</i>	<i>gibbosus</i>		GenBank	Buthidae
KT716037.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
KX648425.1	n/a	<i>Hottentotta</i>	<i>minax</i>		GenBank	Buthidae
KX648429.1	n/a	<i>Compsobuthus</i>	<i>weneri</i>		GenBank	Buthidae
KY982184.1	n/a	<i>Centruroides</i>	<i>schmidtii</i>		GenBank	Buthidae
KY982185.1	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
KY982187.1	n/a	<i>Heteroctenus</i>	<i>abudi</i>		GenBank	Buthidae
KY982188.1	n/a	<i>Heteroctenus</i>	<i>abudi</i>		GenBank	Buthidae
KY982192.1	n/a	<i>Heteroctenus</i>	<i>junceus</i>		GenBank	Buthidae

Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
KY982193.1	n/a	<i>Heteroctenus</i>	<i>junceus</i>		GenBank	Buthidae
KY982194.1	n/a	<i>Heteroctenus</i>	<i>junceus</i>		GenBank	Buthidae
KY982199.1	n/a	<i>Heteroctenus</i>	<i>junceus</i>		GenBank	Buthidae
KY982273.1	n/a	<i>Zabius</i>	<i>fuscus</i>		GenBank	Buthidae
MF422313.1	n/a	<i>Isometrus</i>	sp.		GenBank	Buthidae
MF422319.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422320.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422321.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422322.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422326.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422327.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422328.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422329.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MF422330.1	n/a	<i>Lychas</i>	<i>tricarinatus</i>		GenBank	Buthidae
MK479161.1	n/a	<i>Centruroides</i>	<i>arctimanus</i>		GenBank	Buthidae
MK479165.1	n/a	<i>Centruroides</i>	<i>barbudensis</i>		GenBank	Buthidae
MK479171.1	n/a	<i>Centruroides</i>	<i>exilimanus</i>		GenBank	Buthidae
MK479180.1	n/a	<i>Centruroides</i>	<i>insulanus</i>		GenBank	Buthidae
MK479188.1	n/a	<i>Centruroides</i>	<i>morenoi</i>		GenBank	Buthidae
MK479196.1	n/a	<i>Centruroides</i>	<i>platnicki</i>		GenBank	Buthidae
MK479202.1	n/a	<i>Centruroides</i>	<i>simplex</i>		GenBank	Buthidae
MK479204.1	n/a	<i>Centruroides</i>	<i>taino</i>		GenBank	Buthidae
MK479207.1	n/a	<i>Centruroides</i>	<i>testaceus</i>		GenBank	Buthidae
MK479210.1	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
NC3722.1	n/a	<i>Centruroides</i>	<i>vittatus</i>		GenBank	Buthidae
JN018156.1	n/a	<i>Belisarius</i>	<i>xambeui</i>	MNHN JAD29	GenBank	Troglotayosicidae
JN018163.1	n/a	<i>Chaerilus</i>	<i>julietteae</i>	MNHN JAB32	GenBank	Chaerilidae
HM418309.1	n/a	<i>Iurus</i>	<i>kinzelbachi</i>	VF 0846 1	GenBank	Luridae

Helix ID	Bank accession Num	Genus	Species	Voucher	Source	Family
KF548118.1	n/a	<i>Opisthacanthus</i>	<i>asper</i>	Sc1087	GenBank	Homuridae





		1	2	3	4	5	6	7	8	9	10	11
1	PP01		0.020	0.016	0.020	0.016	0.016	0.021	0.021	0.015	0.015	0.016
2	PP02	0.167		0.019	0.019	0.019	0.019	0.020	0.020	0.019	0.019	0.020
3	PP03	0.101	0.156		0.019	0.003	0.003	0.020	0.020	0.017	0.016	0.018
4	PP04	0.178	0.162	0.148		0.019	0.019	0.018	0.021	0.020	0.020	0.021
5	PP05	0.104	0.156	0.003	0.151		0.000	0.021	0.020	0.017	0.016	0.017
6	PP06	0.104	0.156	0.003	0.151	0.000		0.021	0.020	0.017	0.016	0.017
7	NAD_N93_AC10	0.208	0.178	0.189	0.132	0.192	0.192		0.022	0.021	0.021	0.021
8	NAI_N8_AD1	0.203	0.186	0.170	0.192	0.173	0.173	0.216		0.021	0.021	0.021
9	NAW_N6_AD429	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200		0.014	0.013
10	NAZ_N6_AD457	0.096	0.164	0.110	0.167	0.107	0.107	0.203	0.205	0.082		0.014
11	NBC_N6_AD577	0.101	0.173	0.129	0.195	0.126	0.126	0.211	0.208	0.063	0.077	
12	NBE_N46_AD583	0.189	0.192	0.178	0.140	0.181	0.181	0.153	0.192	0.195	0.200	0.192
13	NBF_N11_AD592	0.184	0.162	0.164	0.173	0.167	0.167	0.205	0.159	0.178	0.167	0.184
14	NBR_N14_AD746	0.164	0.173	0.181	0.186	0.184	0.184	0.205	0.189	0.173	0.175	0.178
15	NBT_N7_AD748	0.107	0.164	0.115	0.173	0.112	0.112	0.216	0.173	0.107	0.112	0.123
16	NBU_N15_AD753	0.164	0.178	0.153	0.167	0.156	0.156	0.208	0.178	0.170	0.142	0.156
17	NBW_N50_AD784	0.170	0.178	0.167	0.159	0.170	0.170	0.197	0.211	0.181	0.178	0.178
18	NBY_N13_AF26b	0.181	0.203	0.167	0.225	0.164	0.164	0.230	0.200	0.200	0.189	0.195
19	NCU_N110_O211	0.181	0.167	0.126	0.159	0.129	0.129	0.203	0.186	0.164	0.145	0.164
20	NCW_N66_O280	0.148	0.153	0.137	0.167	0.140	0.140	0.192	0.159	0.142	0.151	0.153
21	NCY_N67_O282	0.162	0.164	0.148	0.205	0.145	0.145	0.230	0.186	0.137	0.167	0.153
22	NCZ_N110_O285	0.184	0.159	0.140	0.170	0.137	0.137	0.186	0.181	0.145	0.137	0.153
23	NDC_N84_O288	0.197	0.153	0.192	0.189	0.189	0.189	0.225	0.208	0.189	0.181	0.200
24	NDD_N101_O292	0.159	0.164	0.167	0.181	0.164	0.164	0.197	0.184	0.151	0.159	0.156
25	NDG_N78_O304	0.164	0.195	0.142	0.186	0.140	0.140	0.233	0.208	0.145	0.140	0.151
26	NDK_N94_O333	0.189	0.175	0.184	0.123	0.186	0.186	0.164	0.197	0.178	0.173	0.195
27	NDL_N96_O334	0.195	0.181	0.192	0.121	0.195	0.195	0.159	0.208	0.178	0.189	0.181
28	NEH_N112_BI22	0.118	0.153	0.104	0.173	0.101	0.101	0.219	0.173	0.126	0.123	0.126
29	NEM_N43_DW15	0.203	0.181	0.181	0.134	0.178	0.178	0.167	0.219	0.189	0.186	0.203
30	NEM_N43_AT53	0.200	0.184	0.178	0.132	0.175	0.175	0.170	0.216	0.186	0.189	0.200
31	NEN_N115_AD594	0.184	0.178	0.173	0.184	0.170	0.170	0.211	0.173	0.184	0.173	0.167
32	NFN_N43_CG5	0.192	0.200	0.181	0.134	0.184	0.184	0.151	0.216	0.200	0.200	0.208
33	NFZ_N122_BV095	0.197	0.184	0.197	0.159	0.200	0.200	0.153	0.203	0.189	0.186	0.189
34	NGE_N130_CW14	0.189	0.175	0.175	0.118	0.178	0.178	0.134	0.211	0.159	0.170	0.159
35	NGQ_N134_DG3	0.178	0.164	0.162	0.134	0.164	0.164	0.164	0.211	0.186	0.162	0.167
36	NGS_N136_DG10	0.148	0.167	0.151	0.184	0.148	0.148	0.219	0.184	0.159	0.145	0.156

		1	2	3	4	5	6	7	8	9	10	11
37	NRC N150 PC15	0.162	0.170	0.167	0.129	0.170	0.170	0.175	0.186	0.167	0.164	0.170
38	NRF N7 NN11	0.115	0.162	0.110	0.170	0.107	0.107	0.214	0.181	0.110	0.115	0.118
39	NRG N7 NN15	0.118	0.156	0.110	0.170	0.107	0.107	0.214	0.186	0.101	0.118	0.121
40	NRH N7 NN16	0.129	0.162	0.123	0.178	0.121	0.121	0.214	0.195	0.104	0.129	0.129
41	NRI N7 NN17	0.123	0.159	0.121	0.175	0.118	0.118	0.216	0.189	0.104	0.126	0.129
42	NRJ N7 NN18	0.126	0.159	0.121	0.173	0.118	0.118	0.216	0.192	0.101	0.126	0.126
43	NRK N7 NN20	0.110	0.164	0.118	0.181	0.115	0.115	0.219	0.184	0.096	0.126	0.115
44	NRL N7 NN21	0.115	0.159	0.112	0.175	0.110	0.110	0.214	0.181	0.096	0.126	0.115
45	NRM N7 NN37	0.129	0.184	0.132	0.195	0.129	0.129	0.227	0.197	0.118	0.142	0.140
46	NRO N7 NN38	0.110	0.159	0.112	0.178	0.110	0.110	0.216	0.181	0.096	0.126	0.115
47	NRP N138 NN35	0.112	0.142	0.112	0.181	0.115	0.115	0.192	0.175	0.112	0.126	0.121
48	NRQ N138 NN36	0.112	0.145	0.112	0.181	0.115	0.115	0.195	0.178	0.115	0.132	0.126
49	NRZ N147 PC18	0.167	0.148	0.140	0.148	0.142	0.142	0.189	0.184	0.151	0.145	0.170
50	NSA N148 PC16	0.005	0.164	0.104	0.181	0.107	0.107	0.211	0.205	0.088	0.093	0.099
51	NSB N149 PC26	0.088	0.159	0.104	0.175	0.107	0.107	0.197	0.200	0.110	0.099	0.110
52	NSD N151 PC13	0.181	0.162	0.142	0.022	0.145	0.145	0.140	0.195	0.175	0.159	0.192
53	NY N37 AR64	0.186	0.173	0.175	0.148	0.173	0.173	0.148	0.184	0.175	0.178	0.189
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.175	0.189	0.189	0.134	0.192	0.192	0.145	0.208	0.181	0.167	0.173
55	T108978 <i>Aname</i> MYG214 NHC	0.167	0.159	0.153	0.164	0.153	0.153	0.192	0.192	0.148	0.159	0.162
56	T112084 <i>Synothele</i> MYG127 NHD	0.145	0.178	0.140	0.189	0.142	0.142	0.208	0.178	0.153	0.153	0.151
57	T112949 <i>Aname</i> MYG227 NHG	0.140	0.186	0.129	0.173	0.132	0.132	0.205	0.184	0.156	0.156	0.156
58	T96570 <i>Aname</i> MYG067 NHF	0.162	0.186	0.164	0.197	0.162	0.162	0.225	0.195	0.159	0.156	0.159
59	T98767 <i>Aname</i> MYG102 NHI	0.167	0.167	0.142	0.181	0.145	0.145	0.195	0.167	0.167	0.175	0.173
60	T98900 <i>Aname</i> MYG034 NHJ	0.090	0.167	0.129	0.186	0.126	0.126	0.208	0.200	0.055	0.093	0.079
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.132	0.164	0.126	0.184	0.123	0.123	0.211	0.195	0.126	0.118	0.118
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.167	0.148	0.142	0.129	0.145	0.145	0.181	0.186	0.175	0.151	0.167
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.167	0.142	0.137	0.126	0.140	0.140	0.181	0.189	0.175	0.148	0.162
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.107	0.164	0.115	0.173	0.112	0.112	0.216	0.173	0.107	0.112	0.123
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.110	0.173	0.118	0.181	0.115	0.115	0.216	0.184	0.118	0.129	0.137
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.173	0.148	0.175	0.173	0.178	0.178	0.200	0.178	0.162	0.164	0.162
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.170	0.145	0.142	0.129	0.145	0.145	0.181	0.186	0.178	0.153	0.167
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.167	0.145	0.140	0.129	0.142	0.142	0.181	0.189	0.175	0.151	0.164
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.173	0.145	0.148	0.129	0.151	0.151	0.178	0.189	0.175	0.148	0.162
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.167	0.145	0.137	0.132	0.140	0.140	0.184	0.186	0.175	0.151	0.162
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.184	0.170	0.184	0.137	0.186	0.186	0.140	0.200	0.167	0.175	0.175
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.115	0.151	0.101	0.170	0.099	0.099	0.216	0.170	0.123	0.121	0.123

		1	2	3	4	5	6	7	8	9	10	11
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.115	0.151	0.101	0.170	0.099	0.099	0.216	0.170	0.123	0.121	0.123
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.112	0.153	0.104	0.173	0.101	0.101	0.219	0.170	0.121	0.118	0.121
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.118	0.153	0.104	0.173	0.101	0.101	0.219	0.173	0.126	0.123	0.126
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.115	0.148	0.096	0.170	0.093	0.093	0.203	0.167	0.121	0.118	0.115
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.115	0.151	0.096	0.173	0.093	0.093	0.205	0.164	0.118	0.121	0.118
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.170	0.134	0.134	0.118	0.137	0.137	0.170	0.175	0.170	0.151	0.170
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.173	0.151	0.148	0.132	0.151	0.151	0.181	0.192	0.178	0.156	0.167
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.184	0.159	0.148	0.134	0.151	0.151	0.195	0.200	0.186	0.153	0.167
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.186	0.162	0.151	0.134	0.153	0.153	0.192	0.203	0.189	0.156	0.178
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.189	0.162	0.153	0.140	0.156	0.156	0.197	0.205	0.192	0.159	0.181
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.167	0.151	0.140	0.132	0.142	0.142	0.178	0.189	0.175	0.151	0.164
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200	0.000	0.082	0.063
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200	0.000	0.082	0.063
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200	0.000	0.082	0.063
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.195	0.181	0.192	0.121	0.195	0.195	0.159	0.208	0.178	0.189	0.181
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200	0.000	0.082	0.063
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.088	0.159	0.137	0.189	0.134	0.134	0.214	0.205	0.030	0.093	0.077
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.090	0.148	0.126	0.181	0.123	0.123	0.203	0.200	0.000	0.082	0.063
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.101	0.173	0.129	0.195	0.126	0.126	0.211	0.208	0.063	0.077	0.000
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.189	0.192	0.178	0.140	0.181	0.181	0.153	0.192	0.195	0.200	0.192
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.178	0.156	0.153	0.181	0.151	0.151	0.211	0.170	0.148	0.170	0.148
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.090	0.167	0.129	0.186	0.126	0.126	0.208	0.200	0.055	0.093	0.079
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.115	0.167	0.110	0.175	0.107	0.107	0.216	0.170	0.107	0.107	0.118
96	EU404114 <i>Centruroides vittatus</i>	0.274	0.238	0.260	0.255	0.263	0.263	0.274	0.285	0.263	0.252	0.258
97	JF700146 <i>Mesobuthus martensii</i>	0.277	0.252	0.271	0.247	0.268	0.268	0.249	0.293	0.258	0.271	0.277
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.227	0.200	0.205	0.189	0.208	0.208	0.219	0.241	0.236	0.222	0.222

		12	13	14	15	16	17	18	19	20	21	22
1	PP01	0.020	0.020	0.019	0.016	0.019	0.020	0.020	0.020	0.019	0.019	0.020
2	PP02	0.021	0.019	0.020	0.019	0.020	0.020	0.021	0.020	0.019	0.019	0.019
3	PP03	0.020	0.019	0.020	0.017	0.019	0.020	0.020	0.017	0.018	0.019	0.018
4	PP04	0.018	0.020	0.020	0.020	0.020	0.019	0.022	0.019	0.020	0.021	0.020
5	PP05	0.020	0.020	0.020	0.017	0.019	0.020	0.019	0.018	0.018	0.018	0.018
6	PP06	0.020	0.020	0.020	0.017	0.019	0.020	0.019	0.018	0.018	0.018	0.018
7	NAD_N93_AC10	0.019	0.021	0.021	0.022	0.021	0.021	0.022	0.021	0.021	0.022	0.020
8	NAI_N8_AD1	0.021	0.019	0.020	0.020	0.020	0.021	0.021	0.020	0.019	0.020	0.020
9	NAW_N6_AD429	0.021	0.020	0.020	0.016	0.020	0.020	0.021	0.019	0.018	0.018	0.018
10	NAZ_N6_AD457	0.021	0.020	0.020	0.017	0.018	0.020	0.020	0.018	0.019	0.020	0.018
11	NBC_N6_AD577	0.021	0.020	0.020	0.017	0.019	0.020	0.021	0.019	0.019	0.019	0.019
12	NBE_N46_AD583		0.021	0.020	0.021	0.019	0.021	0.022	0.020	0.021	0.021	0.020
13	NBF_N11_AD592	0.205		0.020	0.019	0.021	0.021	0.021	0.020	0.019	0.021	0.020
14	NBR_N14_AD746	0.184	0.167		0.019	0.017	0.020	0.021	0.020	0.019	0.021	0.020
15	NBT_N7_AD748	0.205	0.159	0.164		0.019	0.020	0.020	0.020	0.017	0.019	0.019
16	NBU_N15_AD753	0.159	0.200	0.112	0.164		0.019	0.020	0.020	0.019	0.020	0.019
17	NBW_N50_AD784	0.192	0.192	0.175	0.181	0.162		0.021	0.020	0.020	0.022	0.021
18	NBY_N13_AF26b	0.219	0.195	0.211	0.175	0.175	0.211		0.020	0.020	0.020	0.019
19	NCU_N110_O211	0.184	0.178	0.184	0.167	0.167	0.181	0.181		0.016	0.018	0.013
20	NCW_N66_O280	0.200	0.159	0.159	0.126	0.162	0.184	0.181	0.104		0.018	0.016
21	NCY_N67_O282	0.211	0.208	0.197	0.156	0.178	0.216	0.181	0.137	0.137		0.018
22	NCZ_N110_O285	0.181	0.173	0.178	0.162	0.151	0.195	0.159	0.068	0.110	0.134	
23	NDC_N84_O288	0.197	0.151	0.175	0.186	0.186	0.197	0.225	0.178	0.173	0.205	0.156
24	NDD_N101_O292	0.189	0.175	0.192	0.178	0.181	0.173	0.164	0.156	0.159	0.164	0.162
25	NDG_N78_O304	0.203	0.205	0.197	0.167	0.170	0.184	0.186	0.145	0.153	0.159	0.164
26	NDK_N94_O333	0.159	0.181	0.203	0.189	0.189	0.184	0.216	0.186	0.181	0.205	0.153
27	NDL_N96_O334	0.162	0.197	0.208	0.200	0.203	0.178	0.247	0.181	0.186	0.222	0.195
28	NEH_N112_BI22	0.192	0.156	0.178	0.101	0.164	0.178	0.181	0.153	0.137	0.148	0.142
29	NEM_N43_DW15	0.186	0.211	0.189	0.203	0.205	0.197	0.222	0.200	0.192	0.211	0.181
30	NEM_N43_AT53	0.184	0.214	0.186	0.197	0.203	0.200	0.219	0.203	0.195	0.208	0.184
31	NEN_N115_AD594	0.184	0.181	0.192	0.184	0.170	0.197	0.186	0.156	0.167	0.195	0.167
32	NFN_N43_CG5	0.189	0.203	0.186	0.208	0.203	0.192	0.216	0.197	0.189	0.216	0.200
33	NFZ_N122_BV095	0.162	0.203	0.197	0.197	0.181	0.148	0.227	0.189	0.175	0.216	0.167
34	NGE_N130_CW14	0.148	0.195	0.192	0.195	0.170	0.192	0.211	0.181	0.181	0.197	0.167
35	NGQ_N134_DG3	0.156	0.205	0.173	0.189	0.181	0.186	0.214	0.167	0.167	0.195	0.178
36	NGS_N136_DG10	0.184	0.186	0.178	0.134	0.181	0.203	0.214	0.186	0.164	0.175	0.184

		12	13	14	15	16	17	18	19	20	21	22
37	NRC N150 PC15	0.151	0.200	0.178	0.167	0.192	0.178	0.214	0.167	0.162	0.186	0.159
38	NRF N7 NN11	0.214	0.156	0.181	0.047	0.173	0.156	0.184	0.156	0.123	0.153	0.156
39	NRG N7 NN15	0.214	0.156	0.178	0.038	0.175	0.159	0.175	0.153	0.121	0.148	0.148
40	NRH N7 NN16	0.216	0.167	0.192	0.049	0.189	0.175	0.184	0.164	0.123	0.162	0.151
41	NRI N7 NN17	0.219	0.167	0.186	0.047	0.184	0.167	0.178	0.162	0.123	0.162	0.156
42	NRJ N7 NN18	0.219	0.162	0.189	0.047	0.186	0.170	0.181	0.162	0.121	0.159	0.153
43	NRK N7 NN20	0.216	0.164	0.170	0.047	0.175	0.167	0.192	0.162	0.121	0.148	0.159
44	NRL N7 NN21	0.211	0.159	0.170	0.047	0.170	0.167	0.192	0.162	0.115	0.148	0.153
45	NRM N7 NN37	0.230	0.164	0.186	0.063	0.195	0.189	0.195	0.162	0.129	0.164	0.159
46	NRO N7 NN38	0.216	0.159	0.167	0.047	0.170	0.162	0.192	0.156	0.115	0.142	0.153
47	NRP N138 NN35	0.170	0.181	0.186	0.137	0.175	0.192	0.175	0.164	0.148	0.153	0.140
48	NRQ N138 NN36	0.173	0.186	0.189	0.137	0.178	0.197	0.178	0.170	0.153	0.159	0.148
49	NRZ N147 PC18	0.181	0.186	0.189	0.162	0.153	0.173	0.200	0.137	0.164	0.164	0.156
50	NSA N148 PC16	0.192	0.181	0.167	0.110	0.167	0.167	0.184	0.175	0.145	0.159	0.181
51	NSB N149 PC26	0.178	0.178	0.170	0.115	0.159	0.173	0.197	0.151	0.145	0.156	0.142
52	NSD N151 PC13	0.140	0.170	0.181	0.173	0.164	0.159	0.214	0.153	0.175	0.200	0.164
53	NY N37 AR64	0.159	0.197	0.178	0.192	0.175	0.186	0.205	0.173	0.170	0.203	0.156
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.151	0.203	0.195	0.195	0.170	0.186	0.216	0.186	0.186	0.222	0.181
55	T108978 <i>Aname</i> MYG214 NHC	0.200	0.170	0.181	0.153	0.192	0.173	0.219	0.164	0.153	0.175	0.153
56	T112084 <i>Synothele</i> MYG127 NHD	0.195	0.192	0.178	0.156	0.178	0.192	0.184	0.162	0.132	0.173	0.167
57	T112949 <i>Aname</i> MYG227 NHG	0.170	0.186	0.178	0.151	0.178	0.184	0.164	0.153	0.140	0.181	0.153
58	T96570 <i>Aname</i> MYG067 NHF	0.205	0.195	0.178	0.164	0.175	0.192	0.181	0.156	0.156	0.162	0.153
59	T98767 <i>Aname</i> MYG102 NHI	0.200	0.162	0.145	0.140	0.173	0.195	0.170	0.140	0.126	0.170	0.148
60	T98900 <i>Aname</i> MYG034 NHJ	0.192	0.186	0.173	0.126	0.173	0.184	0.205	0.167	0.142	0.162	0.156
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.184	0.159	0.153	0.115	0.153	0.186	0.189	0.156	0.148	0.175	0.142
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.151	0.178	0.184	0.164	0.148	0.178	0.186	0.145	0.140	0.167	0.148
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.151	0.178	0.178	0.164	0.145	0.181	0.186	0.145	0.148	0.173	0.153
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.205	0.159	0.164	0.000	0.164	0.181	0.175	0.167	0.126	0.156	0.162
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.216	0.164	0.167	0.019	0.181	0.178	0.181	0.164	0.129	0.159	0.164
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.173	0.192	0.197	0.170	0.186	0.186	0.208	0.167	0.178	0.170	0.186
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.153	0.181	0.184	0.164	0.148	0.178	0.189	0.148	0.145	0.170	0.151
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.153	0.181	0.181	0.164	0.148	0.178	0.186	0.145	0.148	0.167	0.148
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.159	0.173	0.181	0.167	0.151	0.184	0.186	0.145	0.148	0.175	0.148
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.156	0.181	0.181	0.162	0.142	0.181	0.195	0.151	0.142	0.178	0.159
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.110	0.195	0.184	0.197	0.164	0.173	0.222	0.208	0.195	0.219	0.197
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.195	0.153	0.175	0.099	0.167	0.175	0.178	0.151	0.134	0.145	0.140

		12	13	14	15	16	17	18	19	20	21	22
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.195	0.153	0.175	0.099	0.167	0.175	0.178	0.151	0.134	0.145	0.140
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.197	0.156	0.178	0.096	0.170	0.178	0.175	0.153	0.137	0.148	0.142
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.192	0.156	0.178	0.101	0.164	0.178	0.181	0.153	0.137	0.148	0.142
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.192	0.140	0.173	0.090	0.159	0.175	0.173	0.145	0.123	0.148	0.134
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.189	0.142	0.175	0.090	0.162	0.178	0.173	0.148	0.126	0.145	0.137
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.151	0.170	0.186	0.167	0.151	0.175	0.186	0.137	0.145	0.167	0.140
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.153	0.178	0.184	0.173	0.148	0.173	0.197	0.148	0.153	0.181	0.153
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.164	0.192	0.181	0.175	0.151	0.184	0.200	0.148	0.162	0.184	0.162
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.164	0.192	0.167	0.184	0.145	0.186	0.203	0.142	0.156	0.181	0.159
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.170	0.192	0.173	0.186	0.151	0.192	0.205	0.145	0.159	0.184	0.162
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.159	0.181	0.175	0.164	0.148	0.184	0.192	0.153	0.148	0.173	0.156
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.195	0.178	0.173	0.107	0.170	0.181	0.200	0.164	0.142	0.137	0.145
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.195	0.178	0.173	0.107	0.170	0.181	0.200	0.164	0.142	0.137	0.145
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.195	0.178	0.173	0.107	0.170	0.181	0.200	0.164	0.142	0.137	0.145
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.162	0.197	0.208	0.200	0.203	0.178	0.247	0.181	0.186	0.222	0.195
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.195	0.178	0.173	0.107	0.170	0.181	0.200	0.164	0.142	0.137	0.145
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.195	0.189	0.175	0.129	0.173	0.178	0.203	0.164	0.148	0.153	0.151
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.195	0.178	0.173	0.107	0.170	0.181	0.200	0.164	0.142	0.137	0.145
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.192	0.184	0.178	0.123	0.156	0.178	0.195	0.164	0.153	0.153	0.153
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.000	0.205	0.184	0.205	0.159	0.192	0.219	0.184	0.200	0.211	0.181
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.197	0.159	0.167	0.167	0.186	0.197	0.197	0.134	0.112	0.164	0.121
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.192	0.186	0.173	0.126	0.173	0.184	0.205	0.167	0.142	0.162	0.156
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.205	0.153	0.173	0.082	0.162	0.175	0.189	0.134	0.115	0.145	0.142
96	EU404114 <i>Centruroides vittatus</i>	0.252	0.255	0.274	0.268	0.277	0.258	0.266	0.252	0.260	0.288	0.260
97	JF700146 <i>Mesobuthus martensii</i>	0.241	0.277	0.268	0.268	0.266	0.249	0.268	0.274	0.271	0.271	0.258
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.225	0.208	0.222	0.222	0.222	0.225	0.225	0.227	0.222	0.219	0.214

		23	24	25	26	27	28	29	30	31	32	33
1	PP01	0.021	0.019	0.019	0.020	0.021	0.017	0.021	0.021	0.020	0.021	0.021
2	PP02	0.019	0.019	0.021	0.020	0.020	0.019	0.020	0.020	0.020	0.021	0.020
3	PP03	0.021	0.020	0.018	0.020	0.021	0.016	0.020	0.020	0.020	0.020	0.021
4	PP04	0.020	0.020	0.020	0.017	0.017	0.020	0.018	0.018	0.020	0.018	0.019
5	PP05	0.020	0.019	0.018	0.020	0.021	0.016	0.020	0.020	0.020	0.020	0.021
6	PP06	0.020	0.019	0.018	0.020	0.021	0.016	0.020	0.020	0.020	0.020	0.021
7	NAD_N93_AC10	0.022	0.021	0.022	0.019	0.019	0.022	0.020	0.020	0.021	0.019	0.019
8	NAI_N8_AD1	0.021	0.020	0.021	0.021	0.021	0.020	0.022	0.022	0.020	0.022	0.021
9	NAW_N6_AD429	0.020	0.019	0.018	0.020	0.020	0.017	0.020	0.020	0.020	0.021	0.020
10	NAZ_N6_AD457	0.020	0.019	0.018	0.020	0.020	0.017	0.020	0.020	0.020	0.021	0.020
11	NBC_N6_AD577	0.021	0.019	0.019	0.021	0.020	0.017	0.021	0.021	0.020	0.021	0.020
12	NBE_N46_AD583	0.021	0.020	0.021	0.019	0.019	0.021	0.020	0.020	0.020	0.020	0.019
13	NBF_N11_AD592	0.019	0.020	0.021	0.020	0.021	0.019	0.021	0.021	0.020	0.021	0.021
14	NBR_N14_AD746	0.020	0.021	0.021	0.021	0.021	0.020	0.020	0.020	0.021	0.020	0.021
15	NBT_N7_AD748	0.020	0.020	0.020	0.020	0.021	0.016	0.021	0.021	0.020	0.021	0.021
16	NBU_N15_AD753	0.020	0.020	0.020	0.020	0.021	0.019	0.021	0.021	0.020	0.021	0.020
17	NBW_N50_AD784	0.021	0.020	0.020	0.020	0.020	0.020	0.021	0.021	0.021	0.021	0.019
18	NBY_N13_AF26b	0.022	0.019	0.020	0.022	0.023	0.020	0.022	0.022	0.020	0.022	0.022
19	NCU_N110_O211	0.020	0.019	0.018	0.020	0.020	0.019	0.021	0.021	0.019	0.021	0.020
20	NCW_N66_O280	0.020	0.019	0.019	0.020	0.020	0.018	0.021	0.021	0.020	0.020	0.020
21	NCY_N67_O282	0.021	0.019	0.019	0.021	0.022	0.019	0.021	0.021	0.021	0.022	0.022
22	NCZ_N110_O285	0.019	0.019	0.019	0.019	0.021	0.018	0.020	0.020	0.020	0.021	0.020
23	NDC_N84_O288		0.021	0.021	0.020	0.021	0.020	0.021	0.021	0.020	0.022	0.021
24	NDD_N101_O292	0.192		0.019	0.021	0.021	0.018	0.020	0.020	0.019	0.020	0.021
25	NDG_N78_O304	0.197	0.148		0.021	0.021	0.019	0.021	0.022	0.020	0.022	0.021
26	NDK_N94_O333	0.178	0.197	0.203		0.018	0.020	0.020	0.020	0.020	0.020	0.019
27	NDL_N96_O334	0.192	0.197	0.214	0.145		0.020	0.020	0.020	0.020	0.020	0.020
28	NEH_N112_BI22	0.175	0.142	0.156	0.175	0.189		0.021	0.021	0.020	0.021	0.021
29	NEM_N43_DW15	0.197	0.178	0.214	0.170	0.178	0.208		0.005	0.021	0.011	0.020
30	NEM_N43_AT53	0.200	0.181	0.216	0.173	0.181	0.203	0.008		0.021	0.011	0.020
31	NEN_N115_AD594	0.181	0.164	0.181	0.186	0.189	0.175	0.195	0.192		0.020	0.021
32	NFN_N43_CG5	0.216	0.175	0.216	0.186	0.178	0.214	0.049	0.047	0.189		0.020
33	NFZ_N122_BV095	0.200	0.197	0.214	0.162	0.170	0.197	0.178	0.175	0.200	0.170	
34	NGE_N130_CW14	0.184	0.184	0.208	0.140	0.126	0.192	0.164	0.167	0.173	0.164	0.170
35	NGQ_N134_DG3	0.211	0.173	0.186	0.153	0.137	0.153	0.148	0.151	0.192	0.137	0.173
36	NGS_N136_DG10	0.189	0.170	0.173	0.214	0.214	0.132	0.208	0.203	0.195	0.208	0.205

		23	24	25	26	27	28	29	30	31	32	33
37	NRC N150 PC15	0.200	0.181	0.200	0.159	0.142	0.178	0.159	0.162	0.184	0.167	0.173
38	NRF N7 NN11	0.184	0.184	0.159	0.173	0.189	0.085	0.208	0.208	0.184	0.214	0.197
39	NRG N7 NN15	0.181	0.186	0.162	0.170	0.189	0.088	0.203	0.203	0.186	0.214	0.197
40	NRH N7 NN16	0.181	0.192	0.170	0.175	0.184	0.096	0.214	0.214	0.195	0.222	0.203
41	NRI N7 NN17	0.181	0.189	0.170	0.175	0.184	0.096	0.208	0.208	0.192	0.216	0.203
42	NRJ N7 NN18	0.184	0.189	0.167	0.175	0.181	0.093	0.208	0.208	0.192	0.216	0.203
43	NRK N7 NN20	0.181	0.181	0.167	0.175	0.186	0.090	0.208	0.205	0.184	0.214	0.205
44	NRL N7 NN21	0.175	0.181	0.167	0.170	0.181	0.085	0.203	0.200	0.184	0.214	0.200
45	NRM N7 NN37	0.186	0.186	0.175	0.197	0.214	0.107	0.211	0.211	0.197	0.214	0.214
46	NRO N7 NN38	0.175	0.175	0.162	0.173	0.184	0.085	0.205	0.203	0.189	0.211	0.205
47	NRP N138 NN35	0.203	0.162	0.170	0.178	0.200	0.129	0.200	0.203	0.178	0.197	0.175
48	NRQ N138 NN36	0.205	0.170	0.175	0.186	0.203	0.129	0.208	0.205	0.178	0.200	0.175
49	NRZ N147 PC18	0.175	0.151	0.159	0.175	0.186	0.151	0.167	0.170	0.178	0.178	0.184
50	NSA N148 PC16	0.195	0.153	0.162	0.186	0.192	0.121	0.200	0.203	0.186	0.195	0.200
51	NSB N149 PC26	0.175	0.178	0.164	0.159	0.192	0.142	0.195	0.197	0.189	0.208	0.192
52	NSD N151 PC13	0.195	0.175	0.195	0.118	0.118	0.164	0.134	0.132	0.173	0.140	0.159
53	NY N37 AR64	0.189	0.173	0.205	0.181	0.156	0.175	0.170	0.167	0.184	0.170	0.156
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.208	0.184	0.205	0.132	0.132	0.181	0.170	0.173	0.200	0.170	0.140
55	T108978 <i>Aname</i> MYG214 NHC	0.181	0.173	0.164	0.173	0.178	0.156	0.197	0.200	0.189	0.211	0.175
56	T112084 <i>Synothele</i> MYG127 NHD	0.195	0.164	0.170	0.203	0.200	0.162	0.192	0.195	0.186	0.173	0.203
57	T112949 <i>Aname</i> MYG227 NHG	0.189	0.148	0.121	0.189	0.197	0.153	0.203	0.200	0.164	0.197	0.200
58	T96570 <i>Aname</i> MYG067 NHF	0.186	0.162	0.126	0.181	0.203	0.156	0.216	0.219	0.173	0.222	0.200
59	T98767 <i>Aname</i> MYG102 NHI	0.175	0.153	0.162	0.184	0.184	0.137	0.200	0.197	0.164	0.200	0.208
60	T98900 <i>Aname</i> MYG034 NHJ	0.192	0.170	0.159	0.189	0.170	0.132	0.195	0.192	0.189	0.197	0.173
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.148	0.162	0.153	0.181	0.181	0.129	0.184	0.186	0.159	0.186	0.200
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.164	0.140	0.164	0.173	0.175	0.153	0.159	0.156	0.126	0.159	0.173
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.156	0.140	0.162	0.170	0.170	0.159	0.162	0.159	0.123	0.162	0.170
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.186	0.178	0.167	0.189	0.200	0.101	0.203	0.197	0.184	0.208	0.197
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.189	0.181	0.167	0.197	0.203	0.110	0.208	0.203	0.186	0.205	0.205
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.175	0.181	0.195	0.162	0.181	0.186	0.197	0.200	0.129	0.203	0.197
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.162	0.140	0.167	0.170	0.170	0.156	0.159	0.156	0.123	0.159	0.167
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.162	0.140	0.167	0.173	0.167	0.156	0.159	0.156	0.121	0.159	0.170
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.162	0.140	0.159	0.170	0.173	0.159	0.164	0.162	0.126	0.164	0.164
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.162	0.142	0.170	0.173	0.175	0.162	0.162	0.159	0.118	0.162	0.173
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.200	0.184	0.205	0.142	0.145	0.195	0.181	0.178	0.208	0.170	0.137
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.173	0.140	0.159	0.173	0.186	0.003	0.205	0.200	0.178	0.211	0.195

		23	24	25	26	27	28	29	30	31	32	33
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.173	0.140	0.159	0.173	0.186	0.003	0.205	0.200	0.178	0.211	0.195
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.175	0.142	0.162	0.175	0.189	0.005	0.208	0.203	0.175	0.214	0.197
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.175	0.142	0.156	0.175	0.189	0.000	0.208	0.203	0.175	0.214	0.197
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.175	0.140	0.162	0.175	0.184	0.025	0.205	0.200	0.170	0.205	0.195
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.178	0.137	0.159	0.173	0.186	0.022	0.205	0.200	0.173	0.205	0.192
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.151	0.134	0.164	0.162	0.162	0.148	0.159	0.156	0.118	0.159	0.167
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.156	0.145	0.175	0.173	0.173	0.159	0.162	0.159	0.123	0.162	0.164
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.170	0.153	0.173	0.181	0.175	0.170	0.175	0.173	0.137	0.175	0.181
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.173	0.153	0.170	0.181	0.175	0.175	0.164	0.156	0.132	0.170	0.189
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.173	0.156	0.173	0.181	0.181	0.178	0.170	0.162	0.132	0.175	0.195
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.164	0.140	0.173	0.175	0.170	0.162	0.156	0.153	0.118	0.156	0.175
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.189	0.151	0.145	0.178	0.178	0.126	0.189	0.186	0.184	0.200	0.189
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.189	0.151	0.145	0.178	0.178	0.126	0.189	0.186	0.184	0.200	0.189
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.189	0.151	0.145	0.178	0.178	0.126	0.189	0.186	0.184	0.200	0.189
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.192	0.197	0.214	0.145	0.000	0.189	0.178	0.181	0.189	0.178	0.170
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.189	0.151	0.145	0.178	0.178	0.126	0.189	0.186	0.184	0.200	0.189
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.192	0.153	0.151	0.186	0.178	0.140	0.195	0.197	0.195	0.200	0.189
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.189	0.151	0.145	0.178	0.178	0.126	0.189	0.186	0.184	0.200	0.189
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.200	0.156	0.151	0.195	0.181	0.126	0.203	0.200	0.167	0.208	0.189
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.197	0.189	0.203	0.159	0.162	0.192	0.186	0.184	0.184	0.189	0.162
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.186	0.162	0.167	0.184	0.197	0.148	0.200	0.203	0.181	0.203	0.200
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.192	0.170	0.159	0.189	0.170	0.132	0.195	0.192	0.189	0.197	0.173
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.186	0.159	0.151	0.175	0.181	0.088	0.195	0.195	0.173	0.200	0.195
96	EU404114 <i>Centruroides vittatus</i>	0.293	0.252	0.255	0.249	0.260	0.260	0.260	0.260	0.277	0.266	0.271
97	JF700146 <i>Mesobuthus martensii</i>	0.277	0.258	0.255	0.249	0.244	0.268	0.258	0.255	0.274	0.249	0.238
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.236	0.197	0.227	0.200	0.216	0.197	0.205	0.203	0.216	0.205	0.233

		34	35	36	37	38	39	40	41	42	43	44
1	PP01	0.020	0.020	0.019	0.019	0.017	0.017	0.018	0.017	0.017	0.016	0.017
2	PP02	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019
3	PP03	0.020	0.019	0.019	0.020	0.016	0.016	0.017	0.017	0.017	0.017	0.017
4	PP04	0.017	0.018	0.020	0.018	0.020	0.020	0.020	0.020	0.020	0.020	0.020
5	PP05	0.020	0.019	0.019	0.020	0.016	0.016	0.017	0.017	0.017	0.017	0.016
6	PP06	0.020	0.019	0.019	0.020	0.016	0.016	0.017	0.017	0.017	0.017	0.016
7	NAD_N93_AC10	0.018	0.019	0.022	0.020	0.021	0.021	0.021	0.022	0.022	0.022	0.021
8	NAI_N8_AD1	0.021	0.021	0.020	0.020	0.020	0.020	0.021	0.020	0.021	0.020	0.020
9	NAW_N6_AD429	0.019	0.020	0.019	0.020	0.016	0.016	0.016	0.016	0.016	0.015	0.015
10	NAZ_N6_AD457	0.020	0.019	0.018	0.019	0.017	0.017	0.018	0.017	0.017	0.017	0.017
11	NBC_N6_AD577	0.019	0.020	0.019	0.020	0.017	0.017	0.018	0.018	0.017	0.017	0.017
12	NBE_N46_AD583	0.019	0.019	0.020	0.019	0.021	0.021	0.022	0.022	0.022	0.022	0.021
13	NBF_N11_AD592	0.021	0.021	0.020	0.021	0.019	0.019	0.020	0.020	0.019	0.019	0.019
14	NBR_N14_AD746	0.021	0.020	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020
15	NBT_N7_AD748	0.021	0.020	0.018	0.020	0.011	0.010	0.011	0.011	0.011	0.011	0.011
16	NBU_N15_AD753	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020
17	NBW_N50_AD784	0.021	0.020	0.021	0.020	0.019	0.019	0.020	0.020	0.020	0.020	0.020
18	NBY_N13_AF26b	0.021	0.021	0.021	0.021	0.020	0.020	0.020	0.020	0.020	0.021	0.021
19	NCU_N110_O211	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019
20	NCW_N66_O280	0.020	0.020	0.019	0.019	0.017	0.017	0.017	0.017	0.017	0.017	0.017
21	NCY_N67_O282	0.021	0.021	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019
22	NCZ_N110_O285	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
23	NDC_N84_O288	0.020	0.021	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020
24	NDD_N101_O292	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020
25	NDG_N78_O304	0.021	0.020	0.020	0.021	0.019	0.019	0.020	0.020	0.020	0.020	0.020
26	NDK_N94_O333	0.018	0.019	0.021	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020
27	NDL_N96_O334	0.017	0.018	0.021	0.018	0.020	0.020	0.020	0.020	0.020	0.020	0.020
28	NEH_N112_BI22	0.021	0.019	0.018	0.020	0.015	0.015	0.015	0.015	0.015	0.015	0.015
29	NEM_N43_DW15	0.019	0.019	0.021	0.019	0.021	0.021	0.021	0.021	0.021	0.021	0.021
30	NEM_N43_AT53	0.020	0.019	0.021	0.019	0.021	0.021	0.021	0.021	0.021	0.021	0.021
31	NEN_N115_AD594	0.020	0.021	0.021	0.020	0.020	0.020	0.021	0.021	0.021	0.020	0.020
32	NFN_N43_CG5	0.019	0.018	0.021	0.020	0.021	0.021	0.022	0.022	0.022	0.021	0.021
33	NFZ_N122_BV095	0.020	0.020	0.021	0.020	0.021	0.021	0.021	0.021	0.021	0.021	0.021
34	NGE_N130_CW14		0.018	0.021	0.018	0.021	0.020	0.020	0.020	0.020	0.020	0.020
35	NGQ_N134_DG3	0.140		0.020	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020
36	NGS_N136_DG10	0.195	0.178		0.021	0.019	0.019	0.020	0.020	0.020	0.019	0.019

		34	35	36	37	38	39	40	41	42	43	44
37	NRC N150 PC15	0.132	0.156	0.203		0.020	0.019	0.020	0.019	0.020	0.020	0.020
38	NRF N7 NN11	0.192	0.181	0.162	0.173		0.005	0.009	0.008	0.008	0.009	0.009
39	NRG N7 NN15	0.186	0.181	0.162	0.164	0.008		0.008	0.006	0.006	0.009	0.009
40	NRH N7 NN16	0.184	0.186	0.170	0.170	0.030	0.022		0.006	0.005	0.010	0.010
41	NRI N7 NN17	0.189	0.184	0.175	0.164	0.022	0.014	0.014		0.004	0.010	0.010
42	NRJ N7 NN18	0.186	0.184	0.173	0.167	0.022	0.014	0.008	0.005		0.009	0.009
43	NRK N7 NN20	0.184	0.178	0.162	0.167	0.033	0.030	0.036	0.038	0.033		0.004
44	NRL N7 NN21	0.184	0.184	0.162	0.167	0.033	0.030	0.036	0.038	0.033	0.005	
45	NRM N7 NN37	0.197	0.197	0.167	0.189	0.060	0.058	0.063	0.066	0.060	0.049	0.055
46	NRO N7 NN38	0.186	0.181	0.156	0.173	0.033	0.030	0.036	0.038	0.033	0.005	0.005
47	NRP N138 NN35	0.170	0.178	0.173	0.159	0.132	0.126	0.132	0.129	0.129	0.137	0.137
48	NRQ N138 NN36	0.178	0.186	0.173	0.167	0.137	0.132	0.129	0.132	0.132	0.142	0.142
49	NRZ N147 PC18	0.153	0.175	0.151	0.175	0.156	0.156	0.170	0.164	0.167	0.167	0.162
50	NSA N148 PC16	0.186	0.175	0.151	0.159	0.112	0.115	0.126	0.121	0.123	0.107	0.112
51	NSB N149 PC26	0.170	0.170	0.164	0.153	0.123	0.121	0.132	0.126	0.129	0.123	0.118
52	NSD N151 PC13	0.115	0.140	0.175	0.126	0.164	0.164	0.173	0.170	0.167	0.175	0.170
53	NY N37 AR64	0.145	0.140	0.205	0.173	0.184	0.181	0.178	0.178	0.175	0.178	0.178
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.129	0.115	0.225	0.159	0.186	0.186	0.186	0.186	0.184	0.184	0.184
55	T108978 <i>Aname</i> MYG214 NHC	0.197	0.186	0.192	0.162	0.151	0.145	0.156	0.151	0.153	0.148	0.142
56	T112084 <i>Synothele</i> MYG127 NHD	0.200	0.164	0.175	0.197	0.151	0.153	0.153	0.153	0.151	0.148	0.153
57	T112949 <i>Aname</i> MYG227 NHG	0.189	0.181	0.167	0.175	0.153	0.156	0.162	0.156	0.159	0.151	0.156
58	T96570 <i>Aname</i> MYG067 NHF	0.181	0.186	0.189	0.189	0.156	0.159	0.167	0.167	0.164	0.148	0.153
59	T98767 <i>Aname</i> MYG102 NHI	0.178	0.167	0.181	0.170	0.140	0.137	0.142	0.142	0.140	0.142	0.137
60	T98900 <i>Aname</i> MYG034 NHJ	0.170	0.175	0.170	0.167	0.126	0.121	0.126	0.123	0.123	0.110	0.110
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.162	0.175	0.145	0.178	0.112	0.115	0.129	0.121	0.126	0.121	0.121
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.153	0.151	0.178	0.153	0.159	0.162	0.170	0.170	0.167	0.181	0.175
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.151	0.151	0.178	0.151	0.162	0.164	0.173	0.170	0.170	0.184	0.178
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.195	0.189	0.134	0.167	0.047	0.038	0.049	0.047	0.047	0.047	0.047
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.203	0.189	0.142	0.170	0.055	0.047	0.058	0.055	0.055	0.049	0.055
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.156	0.162	0.200	0.140	0.167	0.164	0.173	0.170	0.170	0.173	0.173
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.153	0.145	0.181	0.151	0.162	0.164	0.173	0.170	0.170	0.184	0.178
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.151	0.148	0.178	0.148	0.162	0.164	0.173	0.170	0.170	0.184	0.178
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.153	0.151	0.186	0.153	0.164	0.167	0.175	0.173	0.173	0.186	0.181
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.148	0.151	0.175	0.156	0.164	0.167	0.175	0.173	0.173	0.181	0.175
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.129	0.148	0.184	0.153	0.189	0.189	0.186	0.192	0.195	0.189	0.184
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.189	0.151	0.129	0.175	0.082	0.085	0.093	0.093	0.090	0.088	0.082

		34	35	36	37	38	39	40	41	42	43	44
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.189	0.151	0.129	0.175	0.082	0.085	0.093	0.093	0.090	0.088	0.082
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.186	0.148	0.132	0.173	0.079	0.082	0.090	0.090	0.088	0.085	0.085
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.192	0.153	0.132	0.178	0.085	0.088	0.096	0.096	0.093	0.090	0.085
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.175	0.153	0.140	0.170	0.079	0.082	0.096	0.096	0.093	0.085	0.079
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.178	0.156	0.137	0.173	0.079	0.082	0.096	0.096	0.093	0.085	0.079
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.145	0.142	0.181	0.156	0.164	0.167	0.175	0.173	0.173	0.181	0.175
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.156	0.153	0.181	0.156	0.173	0.175	0.186	0.181	0.184	0.186	0.181
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.156	0.162	0.184	0.159	0.170	0.173	0.184	0.178	0.181	0.195	0.189
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.164	0.156	0.192	0.167	0.178	0.181	0.192	0.186	0.189	0.200	0.195
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.159	0.162	0.195	0.173	0.181	0.184	0.195	0.189	0.192	0.203	0.197
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.151	0.151	0.178	0.151	0.167	0.170	0.178	0.175	0.175	0.181	0.175
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.159	0.186	0.159	0.167	0.110	0.101	0.104	0.104	0.101	0.096	0.096
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.159	0.186	0.159	0.167	0.110	0.101	0.104	0.104	0.101	0.096	0.096
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.159	0.186	0.159	0.167	0.110	0.101	0.104	0.104	0.101	0.096	0.096
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.126	0.137	0.214	0.142	0.189	0.189	0.184	0.184	0.181	0.186	0.181
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.159	0.186	0.159	0.167	0.110	0.101	0.104	0.104	0.101	0.096	0.096
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.167	0.181	0.167	0.170	0.129	0.121	0.123	0.123	0.121	0.112	0.118
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.159	0.186	0.159	0.167	0.110	0.101	0.104	0.104	0.101	0.096	0.096
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.159	0.167	0.156	0.170	0.118	0.121	0.129	0.129	0.126	0.115	0.115
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.148	0.156	0.184	0.151	0.214	0.214	0.216	0.219	0.219	0.216	0.211
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.197	0.178	0.159	0.189	0.142	0.145	0.153	0.153	0.151	0.153	0.148
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.170	0.175	0.170	0.167	0.126	0.121	0.126	0.123	0.123	0.110	0.110
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.186	0.162	0.159	0.167	0.066	0.066	0.082	0.079	0.079	0.060	0.066
96	EU404114 <i>Centruroides vittatus</i>	0.268	0.227	0.268	0.249	0.249	0.249	0.266	0.260	0.258	0.258	0.258
97	JF700146 <i>Mesobuthus martensii</i>	0.266	0.244	0.277	0.258	0.279	0.274	0.279	0.282	0.282	0.274	0.274
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.195	0.203	0.230	0.208	0.203	0.205	0.216	0.214	0.211	0.214	0.208

		45	46	47	48	49	50	51	52	53	54	55
1	PP01	0.018	0.016	0.017	0.017	0.020	0.004	0.015	0.020	0.020	0.020	0.020
2	PP02	0.020	0.019	0.018	0.018	0.019	0.019	0.019	0.019	0.020	0.020	0.019
3	PP03	0.018	0.017	0.017	0.017	0.018	0.016	0.016	0.018	0.020	0.020	0.019
4	PP04	0.021	0.020	0.020	0.020	0.019	0.020	0.020	0.008	0.019	0.018	0.019
5	PP05	0.018	0.016	0.017	0.017	0.018	0.016	0.016	0.018	0.020	0.021	0.019
6	PP06	0.018	0.016	0.017	0.017	0.018	0.016	0.016	0.018	0.020	0.021	0.019
7	NAD_N93_AC10	0.022	0.022	0.021	0.021	0.020	0.021	0.021	0.018	0.019	0.018	0.021
8	NAI_N8_AD1	0.021	0.020	0.020	0.020	0.020	0.021	0.021	0.021	0.020	0.021	0.021
9	NAW_N6_AD429	0.017	0.015	0.017	0.017	0.019	0.015	0.016	0.020	0.020	0.020	0.019
10	NAZ_N6_AD457	0.018	0.017	0.017	0.018	0.018	0.015	0.016	0.019	0.020	0.020	0.019
11	NBC_N6_AD577	0.018	0.017	0.017	0.017	0.020	0.016	0.016	0.021	0.020	0.020	0.019
12	NBE_N46_AD583	0.022	0.022	0.020	0.020	0.020	0.021	0.020	0.018	0.019	0.019	0.021
13	NBF_N11_AD592	0.019	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.021	0.020
14	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
15	NBT_N7_AD748	0.013	0.011	0.018	0.018	0.019	0.016	0.017	0.020	0.021	0.021	0.019
16	NBU_N15_AD753	0.021	0.020	0.020	0.020	0.019	0.020	0.019	0.019	0.020	0.020	0.021
17	NBW_N50_AD784	0.020	0.019	0.021	0.021	0.020	0.020	0.020	0.019	0.020	0.020	0.020
18	NBY_N13_AF26b	0.021	0.021	0.020	0.020	0.021	0.020	0.021	0.021	0.021	0.022	0.022
19	NCU_N110_O211	0.019	0.019	0.019	0.020	0.018	0.020	0.019	0.019	0.020	0.020	0.019
20	NCW_N66_O280	0.018	0.017	0.019	0.019	0.019	0.018	0.018	0.020	0.020	0.020	0.019
21	NCY_N67_O282	0.019	0.018	0.019	0.019	0.019	0.019	0.019	0.021	0.021	0.022	0.020
22	NCZ_N110_O285	0.019	0.019	0.018	0.019	0.019	0.020	0.018	0.019	0.019	0.020	0.019
23	NDC_N84_O288	0.020	0.020	0.021	0.021	0.020	0.021	0.020	0.021	0.020	0.021	0.020
24	NDD_N101_O292	0.020	0.020	0.019	0.020	0.019	0.019	0.020	0.020	0.020	0.020	0.020
25	NDG_N78_O304	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.021	0.021	0.021	0.019
26	NDK_N94_O333	0.021	0.020	0.020	0.020	0.020	0.020	0.019	0.017	0.020	0.018	0.020
27	NDL_N96_O334	0.021	0.020	0.021	0.021	0.020	0.021	0.021	0.017	0.019	0.018	0.020
28	NEH_N112_BI22	0.016	0.015	0.018	0.018	0.019	0.017	0.018	0.019	0.020	0.020	0.019
29	NEM_N43_DW15	0.021	0.021	0.021	0.021	0.020	0.021	0.021	0.018	0.020	0.020	0.021
30	NEM_N43_AT53	0.021	0.021	0.021	0.021	0.020	0.021	0.021	0.018	0.020	0.020	0.021
31	NEN_N115_AD594	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
32	NFN_N43_CG5	0.021	0.021	0.021	0.021	0.020	0.021	0.021	0.018	0.020	0.020	0.021
33	NFZ_N122_BV095	0.021	0.021	0.020	0.020	0.020	0.021	0.021	0.019	0.019	0.018	0.020
34	NGE_N130_CW14	0.021	0.020	0.020	0.020	0.019	0.020	0.020	0.017	0.018	0.018	0.021
35	NGQ_N134_DG3	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.018	0.018	0.017	0.020
36	NGS_N136_DG10	0.020	0.019	0.020	0.020	0.019	0.019	0.019	0.020	0.021	0.022	0.021

		45	46	47	48	49	50	51	52	53	54	55
37	NRC N150 PC15	0.020	0.020	0.019	0.020	0.020	0.019	0.019	0.017	0.020	0.019	0.019
38	NRF N7 NN11	0.012	0.009	0.018	0.018	0.019	0.017	0.017	0.019	0.020	0.020	0.019
39	NRG N7 NN15	0.012	0.009	0.017	0.018	0.019	0.017	0.017	0.019	0.020	0.020	0.018
40	NRH N7 NN16	0.013	0.010	0.018	0.018	0.020	0.017	0.018	0.020	0.020	0.020	0.019
41	NRI N7 NN17	0.013	0.010	0.018	0.018	0.019	0.017	0.017	0.020	0.020	0.020	0.019
42	NRJ N7 NN18	0.012	0.009	0.018	0.018	0.020	0.017	0.018	0.020	0.020	0.020	0.019
43	NRK N7 NN20	0.011	0.004	0.018	0.018	0.020	0.016	0.017	0.020	0.020	0.020	0.019
44	NRL N7 NN21	0.012	0.004	0.018	0.018	0.019	0.017	0.017	0.020	0.020	0.020	0.018
45	NRM N7 NN37		0.011	0.019	0.019	0.020	0.017	0.018	0.021	0.021	0.021	0.019
46	NRO N7 NN38	0.049		0.018	0.018	0.019	0.016	0.017	0.020	0.020	0.020	0.018
47	NRP N138 NN35	0.151	0.137		0.005	0.020	0.016	0.017	0.020	0.019	0.020	0.019
48	NRQ N138 NN36	0.156	0.142	0.008		0.020	0.017	0.017	0.020	0.019	0.020	0.020
49	NRZ N147 PC18	0.173	0.162	0.173	0.181		0.019	0.019	0.018	0.020	0.020	0.019
50	NSA N148 PC16	0.126	0.107	0.110	0.115	0.164		0.014	0.020	0.020	0.020	0.020
51	NSB N149 PC26	0.140	0.118	0.121	0.126	0.164	0.082		0.020	0.020	0.020	0.020
52	NSD N151 PC13	0.192	0.173	0.175	0.175	0.140	0.184	0.170		0.019	0.018	0.020
53	NY N37 AR64	0.197	0.181	0.162	0.164	0.186	0.189	0.181	0.151		0.019	0.021
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.203	0.186	0.167	0.175	0.181	0.173	0.173	0.140	0.148		0.020
55	T108978 <i>Aname</i> MYG214 NHC	0.156	0.145	0.162	0.170	0.162	0.167	0.178	0.173	0.192	0.175	
56	T112084 <i>Synothele</i> MYG127 NHD	0.148	0.148	0.145	0.153	0.173	0.142	0.167	0.184	0.184	0.189	0.200
57	T112949 <i>Aname</i> MYG227 NHG	0.151	0.156	0.137	0.134	0.173	0.142	0.156	0.167	0.186	0.192	0.173
58	T96570 <i>Aname</i> MYG067 NHF	0.164	0.153	0.151	0.156	0.151	0.159	0.156	0.181	0.192	0.178	0.195
59	T98767 <i>Aname</i> MYG102 NHI	0.151	0.140	0.164	0.167	0.170	0.170	0.156	0.184	0.170	0.192	0.170
60	T98900 <i>Aname</i> MYG034 NHJ	0.129	0.115	0.115	0.115	0.167	0.093	0.107	0.181	0.156	0.175	0.159
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.123	0.121	0.134	0.142	0.164	0.129	0.123	0.173	0.170	0.175	0.159
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.181	0.175	0.167	0.167	0.145	0.170	0.173	0.129	0.167	0.184	0.184
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.186	0.178	0.162	0.162	0.140	0.170	0.167	0.126	0.164	0.175	0.181
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.063	0.047	0.137	0.137	0.162	0.110	0.115	0.173	0.192	0.195	0.153
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.049	0.049	0.151	0.151	0.173	0.112	0.123	0.181	0.189	0.211	0.159
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.189	0.173	0.159	0.164	0.167	0.170	0.162	0.164	0.192	0.189	0.189
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.184	0.178	0.164	0.164	0.142	0.173	0.173	0.129	0.164	0.181	0.184
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.184	0.178	0.162	0.162	0.142	0.170	0.170	0.126	0.164	0.184	0.181
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.186	0.181	0.164	0.164	0.145	0.175	0.175	0.129	0.164	0.175	0.178
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.184	0.175	0.167	0.167	0.140	0.170	0.167	0.132	0.170	0.184	0.189
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.208	0.184	0.175	0.173	0.148	0.186	0.181	0.140	0.162	0.126	0.184
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.104	0.082	0.126	0.126	0.148	0.118	0.140	0.162	0.173	0.178	0.153

		45	46	47	48	49	50	51	52	53	54	55
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.104	0.082	0.126	0.126	0.148	0.118	0.140	0.162	0.173	0.178	0.153
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.101	0.085	0.123	0.123	0.151	0.115	0.142	0.164	0.170	0.175	0.156
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.107	0.085	0.129	0.129	0.151	0.121	0.142	0.164	0.175	0.181	0.156
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.101	0.079	0.123	0.123	0.153	0.118	0.134	0.167	0.184	0.175	0.151
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.101	0.079	0.121	0.121	0.153	0.118	0.134	0.164	0.184	0.175	0.153
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.181	0.175	0.156	0.156	0.142	0.173	0.164	0.121	0.156	0.167	0.175
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.181	0.181	0.162	0.162	0.142	0.175	0.175	0.132	0.167	0.181	0.181
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.192	0.189	0.175	0.175	0.145	0.186	0.178	0.132	0.178	0.189	0.186
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.195	0.195	0.186	0.186	0.145	0.189	0.167	0.129	0.175	0.192	0.192
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.192	0.197	0.189	0.189	0.148	0.192	0.170	0.134	0.181	0.197	0.197
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.184	0.178	0.167	0.167	0.142	0.170	0.170	0.129	0.167	0.186	0.181
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.118	0.096	0.112	0.115	0.151	0.088	0.110	0.175	0.175	0.181	0.148
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.118	0.096	0.112	0.115	0.151	0.088	0.110	0.175	0.175	0.181	0.148
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.118	0.096	0.112	0.115	0.151	0.088	0.110	0.175	0.175	0.181	0.148
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.214	0.184	0.200	0.203	0.186	0.192	0.192	0.118	0.156	0.132	0.178
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.118	0.096	0.112	0.115	0.151	0.088	0.110	0.175	0.175	0.181	0.148
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.126	0.112	0.115	0.118	0.162	0.085	0.112	0.184	0.178	0.184	0.162
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.118	0.096	0.112	0.115	0.151	0.088	0.110	0.175	0.175	0.181	0.148
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.140	0.115	0.121	0.126	0.170	0.099	0.110	0.192	0.189	0.173	0.162
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.230	0.216	0.170	0.173	0.181	0.192	0.178	0.140	0.159	0.151	0.200
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.159	0.153	0.162	0.170	0.175	0.175	0.159	0.181	0.184	0.197	0.164
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.129	0.115	0.115	0.115	0.167	0.093	0.107	0.181	0.156	0.175	0.159
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.085	0.066	0.132	0.137	0.153	0.112	0.126	0.170	0.175	0.184	0.148
96	EU404114 <i>Centruroides vittatus</i>	0.274	0.255	0.266	0.274	0.244	0.271	0.271	0.249	0.263	0.252	0.266
97	JF700146 <i>Mesobuthus martensii</i>	0.279	0.271	0.252	0.255	0.255	0.279	0.266	0.247	0.258	0.233	0.266
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.233	0.211	0.208	0.211	0.203	0.230	0.219	0.181	0.214	0.216	0.216

		56	57	58	59	60	61	62	63	64	65	66
1	PP01	0.018	0.018	0.019	0.020	0.015	0.018	0.020	0.020	0.016	0.016	0.020
2	PP02	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.018	0.019	0.020	0.019
3	PP03	0.018	0.018	0.019	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.020
4	PP04	0.020	0.020	0.021	0.020	0.020	0.020	0.018	0.017	0.020	0.020	0.020
5	PP05	0.018	0.018	0.019	0.018	0.017	0.017	0.018	0.018	0.017	0.017	0.020
6	PP06	0.018	0.018	0.019	0.018	0.017	0.017	0.018	0.018	0.017	0.017	0.020
7	NAD_N93_AC10	0.021	0.021	0.022	0.021	0.021	0.021	0.020	0.020	0.022	0.022	0.021
8	NAI_N8_AD1	0.020	0.020	0.021	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.020
9	NAW_N6_AD429	0.019	0.019	0.019	0.020	0.012	0.017	0.020	0.020	0.016	0.017	0.019
10	NAZ_N6_AD457	0.019	0.019	0.019	0.020	0.015	0.017	0.019	0.019	0.017	0.018	0.019
11	NBC_N6_AD577	0.019	0.019	0.019	0.020	0.014	0.017	0.020	0.019	0.017	0.018	0.019
12	NBE_N46_AD583	0.021	0.020	0.021	0.021	0.021	0.020	0.019	0.019	0.021	0.022	0.020
13	NBF_N11_AD592	0.021	0.020	0.021	0.019	0.020	0.019	0.020	0.020	0.019	0.019	0.021
14	NBR_N14_AD746	0.020	0.020	0.020	0.018	0.020	0.019	0.020	0.020	0.019	0.020	0.021
15	NBT_N7_AD748	0.019	0.019	0.019	0.018	0.017	0.017	0.019	0.019	0.000	0.007	0.020
16	NBU_N15_AD753	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.018	0.019	0.020	0.020
17	NBW_N50_AD784	0.021	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020
18	NBY_N13_AF26b	0.020	0.019	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.021
19	NCU_N110_O211	0.019	0.019	0.019	0.018	0.020	0.019	0.018	0.018	0.020	0.019	0.020
20	NCW_N66_O280	0.018	0.018	0.019	0.017	0.018	0.019	0.018	0.019	0.017	0.018	0.020
21	NCY_N67_O282	0.020	0.020	0.019	0.020	0.019	0.020	0.020	0.020	0.019	0.019	0.020
22	NCZ_N110_O285	0.020	0.019	0.019	0.019	0.019	0.018	0.019	0.019	0.019	0.019	0.020
23	NDC_N84_O288	0.021	0.020	0.020	0.020	0.021	0.019	0.019	0.019	0.020	0.020	0.020
24	NDD_N101_O292	0.019	0.019	0.019	0.019	0.020	0.019	0.018	0.018	0.020	0.020	0.020
25	NDG_N78_O304	0.020	0.017	0.017	0.019	0.019	0.019	0.019	0.019	0.020	0.020	0.021
26	NDK_N94_O333	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.019
27	NDL_N96_O334	0.021	0.021	0.021	0.020	0.020	0.020	0.020	0.020	0.021	0.021	0.020
28	NEH_N112_BI22	0.019	0.019	0.019	0.018	0.018	0.018	0.019	0.019	0.016	0.016	0.020
29	NEM_N43_DW15	0.021	0.021	0.022	0.021	0.021	0.020	0.019	0.019	0.021	0.021	0.021
30	NEM_N43_AT53	0.021	0.021	0.022	0.021	0.021	0.020	0.019	0.019	0.021	0.021	0.021
31	NEN_N115_AD594	0.020	0.019	0.020	0.019	0.020	0.019	0.017	0.017	0.020	0.020	0.018
32	NFN_N43_CG5	0.020	0.021	0.022	0.021	0.021	0.020	0.019	0.019	0.021	0.021	0.021
33	NFZ_N122_BV095	0.021	0.021	0.021	0.021	0.020	0.021	0.020	0.020	0.021	0.021	0.021
34	NGE_N130_CW14	0.021	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.021	0.021	0.019
35	NGQ_N134_DG3	0.019	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.020	0.020	0.019
36	NGS_N136_DG10	0.020	0.020	0.020	0.020	0.020	0.018	0.020	0.020	0.018	0.018	0.021

		56	57	58	59	60	61	62	63	64	65	66
37	NRC N150 PC15	0.021	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.020	0.020	0.018
38	NRF N7 NN11	0.019	0.019	0.019	0.018	0.017	0.017	0.019	0.019	0.011	0.012	0.020
39	NRG N7 NN15	0.019	0.019	0.019	0.018	0.017	0.017	0.019	0.019	0.010	0.011	0.019
40	NRH N7 NN16	0.019	0.019	0.020	0.018	0.017	0.018	0.020	0.020	0.011	0.012	0.020
41	NRI N7 NN17	0.019	0.019	0.020	0.018	0.017	0.017	0.020	0.020	0.011	0.012	0.020
42	NRJ N7 NN18	0.019	0.019	0.019	0.018	0.017	0.017	0.020	0.020	0.011	0.012	0.020
43	NRK N7 NN20	0.019	0.019	0.019	0.018	0.016	0.017	0.020	0.020	0.011	0.011	0.020
44	NRL N7 NN21	0.019	0.019	0.019	0.018	0.016	0.017	0.020	0.020	0.011	0.012	0.020
45	NRM N7 NN37	0.019	0.019	0.019	0.019	0.018	0.017	0.020	0.020	0.013	0.011	0.020
46	NRO N7 NN38	0.019	0.019	0.019	0.018	0.017	0.017	0.020	0.020	0.011	0.011	0.020
47	NRP N138 NN35	0.018	0.018	0.019	0.019	0.017	0.018	0.020	0.019	0.018	0.019	0.019
48	NRQ N138 NN36	0.019	0.018	0.019	0.020	0.017	0.018	0.020	0.019	0.018	0.019	0.019
49	NRZ N147 PC18	0.020	0.020	0.019	0.020	0.020	0.019	0.018	0.018	0.019	0.020	0.020
50	NSA N148 PC16	0.018	0.018	0.019	0.020	0.015	0.018	0.020	0.020	0.016	0.017	0.020
51	NSB N149 PC26	0.020	0.019	0.019	0.019	0.016	0.017	0.020	0.020	0.017	0.017	0.019
52	NSD N151 PC13	0.020	0.020	0.020	0.020	0.020	0.020	0.018	0.017	0.020	0.020	0.019
53	NY N37 AR64	0.020	0.020	0.021	0.020	0.019	0.020	0.020	0.019	0.021	0.020	0.021
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.020	0.021	0.020	0.021	0.020	0.020	0.020	0.020	0.021	0.021	0.020
55	T108978 <i>Aname</i> MYG214 NHC	0.021	0.020	0.021	0.020	0.019	0.019	0.020	0.020	0.019	0.019	0.020
56	T112084 <i>Synothele</i> MYG127 NHD		0.018	0.018	0.020	0.019	0.018	0.019	0.019	0.019	0.019	0.020
57	T112949 <i>Aname</i> MYG227 NHG	0.145		0.017	0.019	0.019	0.017	0.019	0.019	0.019	0.019	0.020
58	T96570 <i>Aname</i> MYG067 NHF	0.134	0.118		0.019	0.019	0.018	0.020	0.020	0.019	0.020	0.020
59	T98767 <i>Aname</i> MYG102 NHI	0.170	0.153	0.153		0.020	0.019	0.019	0.019	0.018	0.018	0.020
60	T98900 <i>Aname</i> MYG034 NHJ	0.148	0.151	0.153	0.167		0.018	0.020	0.020	0.017	0.018	0.020
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.145	0.126	0.142	0.148	0.129		0.019	0.018	0.017	0.017	0.020
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.151	0.153	0.167	0.151	0.181	0.148		0.006	0.019	0.020	0.017
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.159	0.156	0.175	0.151	0.178	0.142	0.014		0.019	0.020	0.017
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.156	0.151	0.164	0.140	0.126	0.115	0.164	0.164		0.007	0.020
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.162	0.148	0.170	0.140	0.137	0.115	0.173	0.173	0.019		0.020
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.173	0.184	0.181	0.167	0.175	0.181	0.121	0.118	0.170	0.181	
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.151	0.153	0.170	0.153	0.181	0.148	0.005	0.008	0.164	0.173	0.118
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.153	0.156	0.173	0.153	0.178	0.145	0.011	0.008	0.164	0.173	0.115
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.159	0.151	0.175	0.156	0.181	0.148	0.014	0.011	0.167	0.175	0.126
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.153	0.153	0.170	0.151	0.178	0.145	0.014	0.011	0.162	0.170	0.121
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.186	0.189	0.189	0.186	0.162	0.181	0.170	0.162	0.197	0.208	0.186
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.159	0.151	0.153	0.134	0.129	0.126	0.151	0.156	0.099	0.107	0.184

		56	57	58	59	60	61	62	63	64	65	66
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.159	0.151	0.153	0.134	0.129	0.126	0.151	0.156	0.099	0.107	0.184
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.156	0.148	0.151	0.137	0.126	0.123	0.153	0.159	0.096	0.104	0.181
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.162	0.153	0.156	0.137	0.132	0.129	0.153	0.159	0.101	0.110	0.186
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.162	0.142	0.156	0.129	0.132	0.123	0.153	0.159	0.090	0.099	0.178
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.159	0.140	0.153	0.132	0.129	0.121	0.156	0.162	0.090	0.099	0.181
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.148	0.145	0.164	0.148	0.178	0.145	0.016	0.022	0.167	0.175	0.110
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.159	0.162	0.173	0.164	0.175	0.142	0.022	0.025	0.173	0.181	0.129
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.167	0.170	0.184	0.167	0.184	0.153	0.030	0.022	0.175	0.184	0.126
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.175	0.175	0.184	0.162	0.189	0.159	0.036	0.033	0.184	0.192	0.129
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.178	0.178	0.186	0.164	0.192	0.159	0.036	0.033	0.186	0.195	0.134
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.153	0.153	0.170	0.148	0.175	0.145	0.019	0.016	0.164	0.173	0.123
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.153	0.156	0.159	0.167	0.055	0.126	0.175	0.175	0.107	0.118	0.162
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.153	0.156	0.159	0.167	0.055	0.126	0.175	0.175	0.107	0.118	0.162
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.153	0.156	0.159	0.167	0.055	0.126	0.175	0.175	0.107	0.118	0.162
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.200	0.197	0.203	0.184	0.170	0.181	0.175	0.170	0.200	0.203	0.181
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.153	0.156	0.159	0.167	0.055	0.126	0.175	0.175	0.107	0.118	0.162
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.153	0.153	0.151	0.175	0.044	0.134	0.178	0.181	0.129	0.134	0.175
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.153	0.156	0.159	0.167	0.055	0.126	0.175	0.175	0.107	0.118	0.162
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.151	0.156	0.159	0.173	0.079	0.118	0.167	0.162	0.123	0.137	0.162
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.195	0.170	0.205	0.200	0.192	0.184	0.151	0.151	0.205	0.216	0.173
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.145	0.159	0.159	0.151	0.148	0.142	0.178	0.178	0.167	0.170	0.197
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.148	0.151	0.153	0.167	0.000	0.129	0.181	0.178	0.126	0.137	0.175
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.151	0.132	0.148	0.142	0.101	0.121	0.164	0.170	0.082	0.085	0.189
96	EU404114 <i>Centruroides vittatus</i>	0.271	0.255	0.268	0.247	0.271	0.268	0.241	0.244	0.268	0.268	0.249
97	JF700146 <i>Mesobuthus martensii</i>	0.266	0.268	0.252	0.255	0.263	0.263	0.266	0.266	0.268	0.266	0.266
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.230	0.214	0.230	0.208	0.233	0.208	0.181	0.175	0.222	0.230	0.211

		67	68	69	70	71	72	73	74	75	76	77
1	PP01	0.020	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.017	0.017	0.017
2	PP02	0.018	0.018	0.018	0.018	0.020	0.019	0.019	0.019	0.019	0.019	0.019
3	PP03	0.018	0.018	0.019	0.018	0.020	0.016	0.016	0.016	0.016	0.015	0.015
4	PP04	0.018	0.018	0.018	0.018	0.018	0.020	0.020	0.020	0.020	0.020	0.020
5	PP05	0.018	0.018	0.019	0.018	0.020	0.016	0.016	0.016	0.016	0.015	0.015
6	PP06	0.018	0.018	0.019	0.018	0.020	0.016	0.016	0.016	0.016	0.015	0.015
7	NAD_N93_AC10	0.020	0.020	0.020	0.020	0.018	0.022	0.022	0.022	0.022	0.021	0.021
8	NAI_N8_AD1	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.019
9	NAW_N6_AD429	0.020	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.017	0.017	0.017
10	NAZ_N6_AD457	0.019	0.019	0.019	0.019	0.020	0.017	0.017	0.017	0.017	0.017	0.017
11	NBC_N6_AD577	0.020	0.019	0.019	0.019	0.020	0.017	0.017	0.017	0.017	0.017	0.017
12	NBE_N46_AD583	0.019	0.019	0.019	0.019	0.016	0.021	0.021	0.021	0.021	0.021	0.020
13	NBF_N11_AD592	0.020	0.020	0.020	0.020	0.021	0.019	0.019	0.019	0.019	0.018	0.018
14	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
15	NBT_N7_AD748	0.019	0.019	0.020	0.019	0.021	0.016	0.016	0.015	0.016	0.015	0.015
16	NBU_N15_AD753	0.019	0.019	0.019	0.018	0.019	0.020	0.020	0.020	0.019	0.019	0.019
17	NBW_N50_AD784	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
18	NBY_N13_AF26b	0.020	0.020	0.020	0.021	0.022	0.020	0.020	0.020	0.020	0.020	0.020
19	NCU_N110_O211	0.019	0.018	0.018	0.019	0.021	0.019	0.019	0.019	0.019	0.018	0.019
20	NCW_N66_O280	0.018	0.019	0.019	0.018	0.021	0.018	0.018	0.018	0.018	0.017	0.017
21	NCY_N67_O282	0.020	0.020	0.020	0.020	0.022	0.018	0.018	0.019	0.019	0.019	0.018
22	NCZ_N110_O285	0.019	0.019	0.019	0.019	0.021	0.018	0.018	0.018	0.018	0.018	0.018
23	NDC_N84_O288	0.019	0.019	0.019	0.019	0.021	0.020	0.020	0.020	0.020	0.020	0.020
24	NDD_N101_O292	0.018	0.018	0.018	0.018	0.020	0.018	0.018	0.018	0.018	0.018	0.018
25	NDG_N78_O304	0.020	0.020	0.019	0.020	0.021	0.019	0.019	0.019	0.019	0.019	0.019
26	NDK_N94_O333	0.020	0.020	0.020	0.020	0.018	0.020	0.020	0.020	0.020	0.020	0.020
27	NDL_N96_O334	0.020	0.020	0.020	0.020	0.018	0.020	0.020	0.020	0.020	0.020	0.020
28	NEH_N112_BI22	0.019	0.019	0.019	0.019	0.021	0.003	0.003	0.004	0.000	0.008	0.008
29	NEM_N43_DW15	0.019	0.019	0.019	0.019	0.020	0.021	0.021	0.021	0.021	0.021	0.021
30	NEM_N43_AT53	0.019	0.019	0.019	0.019	0.020	0.021	0.021	0.021	0.021	0.021	0.021
31	NEN_N115_AD594	0.017	0.017	0.017	0.017	0.021	0.020	0.020	0.020	0.020	0.020	0.020
32	NFN_N43_CG5	0.019	0.019	0.019	0.019	0.020	0.021	0.021	0.021	0.021	0.021	0.021
33	NFZ_N122_BV095	0.020	0.020	0.019	0.020	0.018	0.021	0.021	0.021	0.021	0.021	0.021
34	NGE_N130_CW14	0.019	0.019	0.019	0.019	0.018	0.020	0.020	0.020	0.021	0.020	0.020
35	NGQ_N134_DG3	0.018	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019
36	NGS_N136_DG10	0.020	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.018	0.018	0.018

		67	68	69	70	71	72	73	74	75	76	77
37	NRC N150 PC15	0.019	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020	0.020
38	NRF N7 NN11	0.019	0.019	0.019	0.019	0.020	0.014	0.014	0.014	0.015	0.014	0.014
39	NRG N7 NN15	0.019	0.019	0.020	0.020	0.020	0.015	0.015	0.014	0.015	0.014	0.014
40	NRH N7 NN16	0.020	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015	0.015
41	NRI N7 NN17	0.020	0.020	0.020	0.020	0.021	0.015	0.015	0.015	0.015	0.015	0.015
42	NRJ N7 NN18	0.020	0.020	0.020	0.020	0.021	0.015	0.015	0.015	0.015	0.015	0.015
43	NRK N7 NN20	0.020	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.015	0.015	0.015
44	NRL N7 NN21	0.020	0.020	0.020	0.020	0.020	0.014	0.014	0.015	0.015	0.014	0.014
45	NRM N7 NN37	0.020	0.020	0.020	0.020	0.021	0.016	0.016	0.016	0.016	0.016	0.016
46	NRO N7 NN38	0.020	0.020	0.020	0.020	0.020	0.014	0.014	0.015	0.015	0.014	0.014
47	NRP N138 NN35	0.019	0.019	0.019	0.020	0.020	0.017	0.017	0.017	0.018	0.017	0.017
48	NRQ N138 NN36	0.019	0.019	0.019	0.020	0.020	0.017	0.017	0.017	0.018	0.017	0.017
49	NRZ N147 PC18	0.018	0.018	0.018	0.018	0.019	0.019	0.019	0.019	0.019	0.019	0.019
50	NSA N148 PC16	0.020	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.017	0.017	0.017
51	NSB N149 PC26	0.020	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.018	0.018	0.018
52	NSD N151 PC13	0.018	0.017	0.018	0.018	0.018	0.019	0.019	0.019	0.019	0.020	0.019
53	NY N37 AR64	0.019	0.019	0.019	0.020	0.019	0.020	0.020	0.020	0.020	0.020	0.020
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.020	0.020	0.020	0.020	0.017	0.020	0.020	0.020	0.020	0.020	0.020
55	T108978 <i>Aname</i> MYG214 NHC	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019
56	T112084 <i>Synothele</i> MYG127 NHD	0.019	0.019	0.019	0.019	0.020	0.019	0.019	0.019	0.019	0.019	0.019
57	T112949 <i>Aname</i> MYG227 NHG	0.019	0.019	0.019	0.019	0.020	0.019	0.019	0.019	0.019	0.018	0.018
58	T96570 <i>Aname</i> MYG067 NHF	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.019	0.019
59	T98767 <i>Aname</i> MYG102 NHI	0.019	0.019	0.019	0.019	0.020	0.018	0.018	0.018	0.018	0.018	0.018
60	T98900 <i>Aname</i> MYG034 NHJ	0.020	0.020	0.020	0.020	0.019	0.018	0.018	0.017	0.018	0.018	0.018
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.019	0.018	0.019	0.018	0.020	0.017	0.017	0.017	0.018	0.017	0.017
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.004	0.005	0.006	0.006	0.020	0.019	0.019	0.019	0.019	0.019	0.019
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.005	0.005	0.005	0.005	0.019	0.019	0.019	0.019	0.019	0.019	0.019
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.019	0.019	0.020	0.019	0.021	0.016	0.016	0.015	0.016	0.015	0.015
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.020	0.020	0.020	0.020	0.021	0.016	0.016	0.016	0.016	0.016	0.016
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.017	0.017	0.017	0.017	0.020	0.020	0.020	0.020	0.020	0.020	0.020
67	KJ744775 <i>Aname mellosa</i> voucher T113629		0.004	0.005	0.005	0.019	0.019	0.019	0.019	0.019	0.019	0.019
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.005		0.006	0.006	0.019	0.019	0.019	0.019	0.019	0.019	0.019
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.008	0.014		0.007	0.020	0.019	0.019	0.019	0.019	0.019	0.019
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.008	0.014	0.016		0.019	0.019	0.019	0.019	0.019	0.019	0.019
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.164	0.164	0.170	0.162		0.021	0.021	0.021	0.021	0.020	0.020
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.153	0.153	0.156	0.159	0.192		0.000	0.003	0.003	0.008	0.007

		67	68	69	70	71	72	73	74	75	76	77
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.153	0.153	0.156	0.159	0.192	0.000		0.003	0.003	0.008	0.007
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.156	0.156	0.159	0.162	0.195	0.003	0.003		0.004	0.008	0.008
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.156	0.156	0.159	0.162	0.195	0.003	0.003	0.005		0.008	0.008
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.156	0.156	0.156	0.156	0.186	0.022	0.022	0.025	0.025		0.003
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.159	0.159	0.159	0.159	0.184	0.019	0.019	0.022	0.022	0.003	
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.014	0.019	0.022	0.022	0.159	0.145	0.145	0.148	0.148	0.148	0.151
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.016	0.022	0.025	0.025	0.153	0.156	0.156	0.159	0.159	0.159	0.162
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.025	0.019	0.033	0.027	0.170	0.167	0.167	0.170	0.170	0.170	0.173
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.036	0.036	0.044	0.038	0.181	0.173	0.173	0.175	0.175	0.175	0.178
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.036	0.036	0.044	0.038	0.181	0.175	0.175	0.178	0.178	0.178	0.181
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.014	0.008	0.022	0.016	0.164	0.159	0.159	0.162	0.162	0.156	0.159
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.178	0.175	0.175	0.175	0.167	0.123	0.123	0.121	0.126	0.121	0.118
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.178	0.175	0.175	0.175	0.167	0.123	0.123	0.121	0.126	0.121	0.118
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.178	0.175	0.175	0.175	0.167	0.123	0.123	0.121	0.126	0.121	0.118
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.170	0.167	0.173	0.175	0.145	0.186	0.186	0.189	0.189	0.184	0.186
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.178	0.175	0.175	0.175	0.167	0.123	0.123	0.121	0.126	0.121	0.118
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.184	0.181	0.184	0.181	0.170	0.137	0.137	0.134	0.140	0.134	0.132
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.178	0.175	0.175	0.175	0.167	0.123	0.123	0.121	0.126	0.121	0.118
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.167	0.164	0.162	0.162	0.175	0.123	0.123	0.121	0.126	0.115	0.118
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.153	0.153	0.159	0.156	0.110	0.195	0.195	0.197	0.192	0.192	0.189
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.178	0.181	0.181	0.178	0.205	0.145	0.145	0.148	0.148	0.142	0.142
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.181	0.178	0.181	0.178	0.162	0.129	0.129	0.126	0.132	0.132	0.129
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.167	0.167	0.167	0.167	0.184	0.085	0.085	0.082	0.088	0.079	0.077
96	EU404114 <i>Centruroides vittatus</i>	0.244	0.247	0.238	0.247	0.241	0.258	0.258	0.260	0.260	0.258	0.255
97	JF700146 <i>Mesobuthus martensii</i>	0.263	0.266	0.266	0.266	0.230	0.266	0.266	0.268	0.268	0.263	0.260
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.181	0.178	0.178	0.186	0.214	0.195	0.195	0.197	0.197	0.195	0.197

		78	79	80	81	82	83	84	85	86	87	88
1	PP01	0.020	0.020	0.020	0.020	0.020	0.020	0.015	0.015	0.015	0.021	0.015
2	PP02	0.018	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.020	0.019
3	PP03	0.018	0.019	0.019	0.019	0.019	0.018	0.017	0.017	0.017	0.021	0.017
4	PP04	0.017	0.018	0.018	0.018	0.018	0.018	0.020	0.020	0.020	0.017	0.020
5	PP05	0.018	0.019	0.019	0.019	0.019	0.018	0.017	0.017	0.017	0.021	0.017
6	PP06	0.018	0.019	0.019	0.019	0.019	0.018	0.017	0.017	0.017	0.021	0.017
7	NAD_N93_AC10	0.020	0.020	0.021	0.021	0.021	0.020	0.021	0.021	0.021	0.019	0.021
8	NAI_N8_AD1	0.020	0.021	0.021	0.021	0.021	0.020	0.021	0.021	0.021	0.021	0.021
9	NAW_N6_AD429	0.020	0.020	0.020	0.020	0.021	0.020	0.000	0.000	0.000	0.020	0.000
10	NAZ_N6_AD457	0.019	0.019	0.019	0.019	0.019	0.019	0.014	0.014	0.014	0.020	0.014
11	NBC_N6_AD577	0.020	0.020	0.020	0.020	0.020	0.019	0.013	0.013	0.013	0.020	0.013
12	NBE_N46_AD583	0.019	0.019	0.019	0.019	0.020	0.019	0.021	0.021	0.021	0.019	0.021
13	NBF_N11_AD592	0.020	0.020	0.021	0.021	0.021	0.020	0.020	0.020	0.020	0.021	0.020
14	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.021	0.020
15	NBT_N7_AD748	0.020	0.020	0.020	0.020	0.020	0.019	0.016	0.016	0.016	0.021	0.016
16	NBU_N15_AD753	0.019	0.019	0.019	0.018	0.019	0.019	0.020	0.020	0.020	0.021	0.020
17	NBW_N50_AD784	0.020	0.020	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.020
18	NBY_N13_AF26b	0.020	0.021	0.021	0.021	0.021	0.021	0.021	0.021	0.021	0.023	0.021
19	NCU_N110_O211	0.018	0.019	0.019	0.018	0.018	0.019	0.019	0.019	0.019	0.020	0.019
20	NCW_N66_O280	0.018	0.019	0.019	0.019	0.019	0.019	0.018	0.018	0.018	0.020	0.018
21	NCY_N67_O282	0.020	0.020	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.022	0.018
22	NCZ_N110_O285	0.018	0.019	0.019	0.019	0.019	0.019	0.018	0.018	0.018	0.021	0.018
23	NDC_N84_O288	0.019	0.019	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.021	0.020
24	NDD_N101_O292	0.018	0.018	0.019	0.019	0.019	0.018	0.019	0.019	0.019	0.021	0.019
25	NDG_N78_O304	0.019	0.020	0.020	0.020	0.020	0.020	0.018	0.018	0.018	0.021	0.018
26	NDK_N94_O333	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.018	0.020
27	NDL_N96_O334	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.000	0.020
28	NEH_N112_BI22	0.019	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
29	NEM_N43_DW15	0.019	0.019	0.020	0.019	0.020	0.019	0.020	0.020	0.020	0.020	0.020
30	NEM_N43_AT53	0.019	0.019	0.020	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020
31	NEN_N115_AD594	0.017	0.017	0.018	0.018	0.018	0.017	0.020	0.020	0.020	0.020	0.020
32	NFN_N43_CG5	0.019	0.019	0.020	0.020	0.020	0.019	0.021	0.021	0.021	0.020	0.021
33	NFZ_N122_BV095	0.020	0.019	0.020	0.020	0.021	0.020	0.020	0.020	0.020	0.020	0.020
34	NGE_N130_CW14	0.018	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.019	0.017	0.019
35	NGQ_N134_DG3	0.018	0.019	0.019	0.019	0.019	0.019	0.020	0.020	0.020	0.018	0.020
36	NGS_N136_DG10	0.020	0.020	0.020	0.021	0.021	0.020	0.019	0.019	0.019	0.021	0.019

		78	79	80	81	82	83	84	85	86	87	88
37	NRC N150 PC15	0.019	0.019	0.019	0.020	0.020	0.019	0.020	0.020	0.020	0.018	0.020
38	NRF N7 NN11	0.019	0.020	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.020	0.016
39	NRG N7 NN15	0.020	0.020	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.020	0.016
40	NRH N7 NN16	0.020	0.020	0.020	0.021	0.021	0.020	0.016	0.016	0.016	0.020	0.016
41	NRI N7 NN17	0.020	0.020	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.020	0.016
42	NRJ N7 NN18	0.020	0.020	0.020	0.020	0.021	0.020	0.016	0.016	0.016	0.020	0.016
43	NRK N7 NN20	0.020	0.020	0.021	0.021	0.021	0.020	0.015	0.015	0.015	0.020	0.015
44	NRL N7 NN21	0.020	0.020	0.020	0.021	0.021	0.020	0.015	0.015	0.015	0.020	0.015
45	NRM N7 NN37	0.020	0.020	0.021	0.021	0.021	0.020	0.017	0.017	0.017	0.021	0.017
46	NRO N7 NN38	0.020	0.020	0.020	0.021	0.021	0.020	0.015	0.015	0.015	0.020	0.015
47	NRP N138 NN35	0.019	0.019	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.021	0.017
48	NRQ N138 NN36	0.019	0.019	0.020	0.020	0.020	0.020	0.017	0.017	0.017	0.021	0.017
49	NRZ N147 PC18	0.018	0.018	0.018	0.018	0.019	0.018	0.019	0.019	0.019	0.020	0.019
50	NSA N148 PC16	0.020	0.020	0.020	0.020	0.021	0.020	0.015	0.015	0.015	0.021	0.015
51	NSB N149 PC26	0.019	0.020	0.020	0.020	0.020	0.020	0.016	0.016	0.016	0.021	0.016
52	NSD N151 PC13	0.017	0.018	0.018	0.018	0.018	0.018	0.020	0.020	0.020	0.017	0.020
53	NY N37 AR64	0.019	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.019	0.020
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.020	0.020	0.020	0.021	0.021	0.020	0.020	0.020	0.020	0.018	0.020
55	T108978 <i>Aname</i> MYG214 NHC	0.020	0.020	0.020	0.021	0.021	0.020	0.019	0.019	0.019	0.020	0.019
56	T112084 <i>Synothele</i> MYG127 NHD	0.019	0.019	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.021	0.019
57	T112949 <i>Aname</i> MYG227 NHG	0.018	0.019	0.020	0.020	0.020	0.019	0.019	0.019	0.019	0.021	0.019
58	T96570 <i>Aname</i> MYG067 NHF	0.019	0.020	0.020	0.020	0.020	0.020	0.019	0.019	0.019	0.021	0.019
59	T98767 <i>Aname</i> MYG102 NHI	0.019	0.019	0.020	0.019	0.019	0.019	0.020	0.020	0.020	0.020	0.020
60	T98900 <i>Aname</i> MYG034 NHJ	0.020	0.020	0.020	0.020	0.021	0.020	0.012	0.012	0.012	0.020	0.012
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.018	0.018	0.019	0.019	0.019	0.018	0.017	0.017	0.017	0.020	0.017
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.007	0.008	0.009	0.010	0.010	0.007	0.020	0.020	0.020	0.020	0.020
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.008	0.008	0.008	0.009	0.009	0.007	0.020	0.020	0.020	0.020	0.020
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.020	0.020	0.020	0.020	0.020	0.019	0.016	0.016	0.016	0.021	0.016
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.020	0.020	0.020	0.021	0.021	0.020	0.017	0.017	0.017	0.021	0.017
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.016	0.018	0.017	0.018	0.018	0.017	0.019	0.019	0.019	0.020	0.019
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.006	0.007	0.008	0.010	0.010	0.006	0.020	0.020	0.020	0.020	0.020
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.007	0.008	0.007	0.010	0.010	0.005	0.020	0.020	0.020	0.020	0.020
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.008	0.008	0.009	0.011	0.011	0.008	0.020	0.020	0.020	0.020	0.020
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.008	0.008	0.009	0.010	0.010	0.007	0.020	0.020	0.020	0.020	0.020
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.019	0.019	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.018	0.020
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.018	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017

		78	79	80	81	82	83	84	85	86	87	88
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.018	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.019	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.019	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.019	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.019	0.019	0.020	0.020	0.020	0.019	0.017	0.017	0.017	0.020	0.017
78	KJ744982 <i>Aname mellosa</i> voucher T122207		0.008	0.009	0.010	0.010	0.009	0.020	0.020	0.020	0.019	0.020
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.025		0.010	0.010	0.010	0.009	0.020	0.020	0.020	0.020	0.020
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.033	0.036		0.009	0.009	0.009	0.020	0.020	0.020	0.020	0.020
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.041	0.041	0.027		0.004	0.011	0.020	0.020	0.020	0.020	0.020
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.041	0.041	0.027	0.005		0.011	0.021	0.021	0.021	0.020	0.021
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.027	0.030	0.027	0.044	0.044		0.020	0.020	0.020	0.020	0.020
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.170	0.178	0.186	0.189	0.192	0.175		0.000	0.000	0.020	0.000
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.170	0.178	0.186	0.189	0.192	0.175	0.000		0.000	0.020	0.000
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.170	0.178	0.186	0.189	0.192	0.175	0.000	0.000		0.020	0.000
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.162	0.173	0.175	0.175	0.181	0.170	0.178	0.178	0.178		0.020
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.170	0.178	0.186	0.189	0.192	0.175	0.000	0.000	0.000	0.178	
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304	0.178	0.184	0.192	0.197	0.200	0.181	0.030	0.030	0.030	0.178	0.030
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.170	0.178	0.186	0.189	0.192	0.175	0.000	0.000	0.000	0.178	0.000
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.170	0.167	0.167	0.178	0.181	0.164	0.063	0.063	0.063	0.181	0.063
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.151	0.153	0.164	0.164	0.170	0.159	0.195	0.195	0.195	0.162	0.195
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.175	0.184	0.186	0.181	0.184	0.184	0.148	0.148	0.148	0.197	0.148
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.178	0.175	0.184	0.189	0.192	0.175	0.055	0.055	0.055	0.170	0.055
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.164	0.170	0.181	0.181	0.184	0.164	0.107	0.107	0.107	0.181	0.107
96	EU404114 <i>Centruroides vittatus</i>	0.244	0.258	0.258	0.252	0.255	0.247	0.263	0.263	0.263	0.260	0.263
97	JF700146 <i>Mesobuthus martensii</i>	0.255	0.268	0.274	0.277	0.282	0.266	0.258	0.258	0.258	0.244	0.258
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.178	0.184	0.186	0.184	0.178	0.181	0.236	0.236	0.236	0.216	0.236

		89	90	91	92	93	94	95	96	97	98
1	PP01	0.015	0.015	0.016	0.020	0.020	0.015	0.017	0.023	0.023	0.022
2	PP02	0.019	0.019	0.020	0.021	0.019	0.020	0.020	0.022	0.023	0.021
3	PP03	0.018	0.017	0.018	0.020	0.019	0.018	0.016	0.023	0.023	0.021
4	PP04	0.020	0.020	0.021	0.018	0.020	0.020	0.020	0.023	0.023	0.020
5	PP05	0.018	0.017	0.017	0.020	0.019	0.017	0.016	0.023	0.023	0.021
6	PP06	0.018	0.017	0.017	0.020	0.019	0.017	0.016	0.023	0.023	0.021
7	NAD_N93_AC10	0.021	0.021	0.021	0.019	0.021	0.021	0.022	0.023	0.023	0.022
8	NAI_N8_AD1	0.021	0.021	0.021	0.021	0.020	0.021	0.020	0.024	0.024	0.022
9	NAW_N6_AD429	0.009	0.000	0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
10	NAZ_N6_AD457	0.015	0.014	0.014	0.021	0.020	0.015	0.016	0.023	0.023	0.022
11	NBC_N6_AD577	0.014	0.013	0.000	0.021	0.019	0.014	0.017	0.023	0.023	0.022
12	NBE_N46_AD583	0.021	0.021	0.021	0.000	0.021	0.021	0.021	0.023	0.022	0.022
13	NBF_N11_AD592	0.020	0.020	0.020	0.021	0.019	0.020	0.019	0.023	0.023	0.021
14	NBR_N14_AD746	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.023	0.023	0.022
15	NBT_N7_AD748	0.018	0.016	0.017	0.021	0.020	0.017	0.014	0.023	0.023	0.022
16	NBU_N15_AD753	0.020	0.020	0.019	0.019	0.020	0.020	0.019	0.023	0.023	0.022
17	NBW_N50_AD784	0.020	0.020	0.020	0.021	0.021	0.020	0.020	0.023	0.023	0.022
18	NBY_N13_AF26b	0.021	0.021	0.021	0.022	0.021	0.021	0.020	0.023	0.023	0.022
19	NCU_N110_O211	0.019	0.019	0.019	0.020	0.018	0.020	0.018	0.023	0.023	0.022
20	NCW_N66_O280	0.019	0.018	0.019	0.021	0.017	0.018	0.017	0.023	0.023	0.022
21	NCY_N67_O282	0.019	0.018	0.019	0.021	0.019	0.019	0.018	0.024	0.023	0.022
22	NCZ_N110_O285	0.019	0.018	0.019	0.020	0.017	0.019	0.018	0.023	0.023	0.021
23	NDC_N84_O288	0.021	0.020	0.021	0.021	0.020	0.021	0.020	0.024	0.023	0.022
24	NDD_N101_O292	0.019	0.019	0.019	0.020	0.019	0.020	0.019	0.023	0.023	0.021
25	NDG_N78_O304	0.019	0.018	0.019	0.021	0.020	0.019	0.019	0.023	0.023	0.022
26	NDK_N94_O333	0.020	0.020	0.021	0.019	0.020	0.020	0.020	0.023	0.023	0.021
27	NDL_N96_O334	0.020	0.020	0.020	0.019	0.021	0.020	0.020	0.023	0.022	0.022
28	NEH_N112_BI22	0.018	0.017	0.017	0.021	0.019	0.018	0.015	0.023	0.023	0.021
29	NEM_N43_DW15	0.021	0.020	0.021	0.020	0.021	0.021	0.021	0.023	0.023	0.021
30	NEM_N43_AT53	0.021	0.020	0.021	0.020	0.021	0.021	0.021	0.023	0.023	0.021
31	NEN_N115_AD594	0.021	0.020	0.020	0.020	0.020	0.020	0.020	0.023	0.023	0.022
32	NFN_N43_CG5	0.021	0.021	0.021	0.020	0.021	0.021	0.021	0.023	0.023	0.021
33	NFZ_N122_BV095	0.020	0.020	0.020	0.019	0.021	0.020	0.021	0.023	0.022	0.022
34	NGE_N130_CW14	0.020	0.019	0.019	0.019	0.021	0.020	0.020	0.023	0.023	0.021
35	NGQ_N134_DG3	0.020	0.020	0.020	0.019	0.020	0.020	0.019	0.022	0.022	0.021
36	NGS_N136_DG10	0.020	0.019	0.019	0.020	0.019	0.020	0.019	0.023	0.023	0.022

		89	90	91	92	93	94	95	96	97	98
37	NRC N150 PC15	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.023	0.023	0.021
38	NRF N7 NN11	0.018	0.016	0.017	0.021	0.018	0.017	0.013	0.023	0.023	0.021
39	NRG N7 NN15	0.017	0.016	0.017	0.021	0.018	0.017	0.013	0.023	0.023	0.021
40	NRH N7 NN16	0.017	0.016	0.018	0.022	0.019	0.017	0.014	0.023	0.023	0.022
41	NRI N7 NN17	0.017	0.016	0.018	0.022	0.019	0.017	0.014	0.023	0.024	0.021
42	NRJ N7 NN18	0.017	0.016	0.017	0.022	0.019	0.017	0.014	0.023	0.024	0.021
43	NRK N7 NN20	0.017	0.015	0.017	0.022	0.019	0.016	0.012	0.023	0.023	0.021
44	NRL N7 NN21	0.017	0.015	0.017	0.021	0.019	0.016	0.013	0.023	0.023	0.021
45	NRM N7 NN37	0.017	0.017	0.018	0.022	0.019	0.018	0.015	0.023	0.023	0.022
46	NRO N7 NN38	0.017	0.015	0.017	0.022	0.019	0.017	0.013	0.023	0.023	0.021
47	NRP N138 NN35	0.017	0.017	0.017	0.020	0.019	0.017	0.018	0.023	0.023	0.021
48	NRQ N138 NN36	0.017	0.017	0.017	0.020	0.020	0.017	0.018	0.023	0.023	0.021
49	NRZ N147 PC18	0.019	0.019	0.020	0.020	0.020	0.020	0.019	0.022	0.023	0.021
50	NSA N148 PC16	0.015	0.015	0.016	0.021	0.020	0.015	0.017	0.023	0.023	0.022
51	NSB N149 PC26	0.017	0.016	0.016	0.020	0.019	0.016	0.017	0.023	0.023	0.022
52	NSD N151 PC13	0.020	0.020	0.021	0.018	0.020	0.020	0.020	0.023	0.023	0.020
53	NY N37 AR64	0.020	0.020	0.020	0.019	0.020	0.019	0.020	0.023	0.023	0.021
54	T101209 <i>Kwonkan</i> MYG175 NHP	0.020	0.020	0.020	0.019	0.021	0.020	0.020	0.023	0.022	0.022
55	T108978 <i>Aname</i> MYG214 NHC	0.019	0.019	0.019	0.021	0.019	0.019	0.019	0.023	0.023	0.022
56	T112084 <i>Synothele</i> MYG127 NHD	0.019	0.019	0.019	0.021	0.018	0.019	0.019	0.023	0.023	0.022
57	T112949 <i>Aname</i> MYG227 NHG	0.019	0.019	0.019	0.020	0.019	0.019	0.018	0.023	0.023	0.021
58	T96570 <i>Aname</i> MYG067 NHF	0.019	0.019	0.019	0.021	0.019	0.019	0.019	0.023	0.023	0.022
59	T98767 <i>Aname</i> MYG102 NHI	0.020	0.020	0.020	0.021	0.019	0.020	0.018	0.023	0.023	0.021
60	T98900 <i>Aname</i> MYG034 NHJ	0.011	0.012	0.014	0.021	0.019	0.000	0.016	0.023	0.023	0.022
61	JQ772139 <i>Aname</i> sp 2 MGR-2012 voucher WAMT98892	0.018	0.017	0.017	0.020	0.018	0.018	0.017	0.023	0.023	0.021
62	KJ744505 <i>Aname mellosa</i> voucher T103199	0.020	0.020	0.020	0.019	0.020	0.020	0.019	0.022	0.023	0.020
63	KJ744623 <i>Aname mellosa</i> voucher T105871	0.020	0.020	0.019	0.019	0.020	0.020	0.020	0.022	0.023	0.020
64	KJ744648 <i>Aname</i> sp MYG373 voucher T107087	0.018	0.016	0.017	0.021	0.020	0.017	0.014	0.023	0.023	0.022
65	KJ744649 <i>Aname</i> sp MYG373 voucher T107089	0.018	0.017	0.018	0.022	0.020	0.018	0.015	0.023	0.023	0.022
66	KJ744677 <i>Aname mellosa</i> voucher T107987	0.020	0.019	0.019	0.020	0.021	0.020	0.020	0.023	0.023	0.021
67	KJ744775 <i>Aname mellosa</i> voucher T113629	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.022	0.023	0.020
68	KJ744785 <i>Aname mellosa</i> voucher T113642	0.020	0.020	0.019	0.019	0.020	0.020	0.020	0.023	0.023	0.020
69	KJ744788 <i>Aname mellosa</i> voucher T113648	0.020	0.020	0.019	0.019	0.020	0.020	0.020	0.022	0.023	0.020
70	KJ744791 <i>Aname mellosa</i> voucher T113654	0.020	0.020	0.019	0.019	0.020	0.020	0.020	0.023	0.023	0.020
71	KJ744833 <i>Kwonkan</i> sp MYG006 voucher T114812	0.020	0.020	0.020	0.016	0.021	0.019	0.020	0.022	0.022	0.021
72	KJ744901 <i>Aname</i> sp MYG331 voucher T118789	0.018	0.017	0.017	0.021	0.018	0.018	0.015	0.023	0.023	0.021

		89	90	91	92	93	94	95	96	97	98
73	KJ744902 <i>Aname</i> sp MYG331 voucher T118791	0.018	0.017	0.017	0.021	0.018	0.018	0.015	0.023	0.023	0.021
74	KJ744909 <i>Aname</i> sp MYG331 voucher T118805	0.018	0.017	0.017	0.021	0.019	0.017	0.014	0.023	0.023	0.021
75	KJ744910 <i>Aname</i> sp MYG331 voucher T118811	0.018	0.017	0.017	0.021	0.019	0.018	0.015	0.023	0.023	0.021
76	KJ744911 <i>Aname</i> sp MYG331 voucher T118812	0.018	0.017	0.017	0.021	0.018	0.018	0.014	0.023	0.023	0.021
77	KJ744914 <i>Aname</i> sp MYG331 voucher T118818	0.018	0.017	0.017	0.020	0.018	0.018	0.014	0.023	0.023	0.021
78	KJ744982 <i>Aname mellosa</i> voucher T122207	0.020	0.020	0.020	0.019	0.020	0.020	0.019	0.022	0.023	0.020
79	KJ744987 <i>Aname mellosa</i> voucher T122215	0.020	0.020	0.020	0.019	0.020	0.020	0.020	0.023	0.023	0.020
80	KJ744989 <i>Aname mellosa</i> voucher T122218	0.021	0.020	0.020	0.019	0.020	0.020	0.020	0.023	0.023	0.020
81	KJ744990 <i>Aname mellosa</i> voucher T122219	0.021	0.020	0.020	0.019	0.020	0.020	0.020	0.023	0.023	0.020
82	KJ744992 <i>Aname mellosa</i> voucher T122222	0.021	0.021	0.020	0.020	0.020	0.021	0.020	0.023	0.024	0.020
83	KJ745155 <i>Aname mellosa</i> voucher T126273	0.020	0.020	0.019	0.019	0.020	0.020	0.019	0.023	0.023	0.020
84	KJ745231 <i>Aname</i> sp MYG351 voucher T74238	0.009	0.000	0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
85	KJ745232 <i>Aname</i> sp MYG351 voucher T74241	0.009	0.000	0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
86	KJ745233 <i>Aname</i> sp MYG351 voucher T74247	0.009	0.000	0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
87	KJ745281 <i>Kwonkan</i> sp MYG361 voucher T78543	0.020	0.020	0.020	0.019	0.021	0.020	0.020	0.023	0.022	0.022
88	KJ745287 <i>Aname</i> sp MYG351 voucher T82303	0.009	0.000	0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
89	KJ745288 <i>Aname</i> sp MYG351 voucher T82304		0.009	0.014	0.021	0.019	0.011	0.017	0.023	0.023	0.022
90	KJ745293 <i>Aname</i> sp MYG351 voucher T82309	0.030		0.013	0.021	0.019	0.012	0.016	0.023	0.023	0.022
91	KJ745375 <i>Aname</i> sp MYG034 voucher T93314	0.077	0.063		0.021	0.019	0.014	0.017	0.023	0.023	0.022
92	KJ745401 <i>Kwonkan</i> sp MYG006 voucher T95405	0.195	0.195	0.192		0.021	0.021	0.021	0.023	0.022	0.022
93	KJ745429 <i>Aname</i> sp MYG030 voucher T96495	0.159	0.148	0.148	0.197		0.019	0.019	0.023	0.023	0.022
94	KJ745494 <i>Aname</i> sp MYG034 voucher T98900	0.044	0.055	0.079	0.192	0.148		0.016	0.023	0.023	0.022
95	MG800157 <i>Aname</i> sp MYG411 voucher WAMT94952	0.112	0.107	0.118	0.205	0.153	0.101		0.022	0.023	0.022
96	EU404114 <i>Centruroides vittatus</i>	0.268	0.263	0.258	0.252	0.258	0.271	0.244		0.020	0.023
97	JF700146 <i>Mesobuthus martensii</i>	0.255	0.258	0.277	0.241	0.274	0.263	0.268	0.167		0.024
98	KJ7447421 <i>Selenotholus</i> sp MYG381 voucher T113579	0.236	0.236	0.222	0.225	0.233	0.233	0.216	0.252	0.285	

		1	2	3	4	5	6	7	8
1	PP07		0.013	0.004	0.007	0.012	0.017	0.007	0.018
2	PP08	0.094		0.013	0.014	0.014	0.017	0.014	0.017
3	PP11	0.008	0.094		0.007	0.012	0.017	0.007	0.018
4	<i>Lychas annulatus</i> clade B PC01	0.024	0.102	0.024		0.012	0.017	0.003	0.018
5	<i>Lychas annulatus</i> clade A PC02	0.072	0.104	0.076	0.076		0.017	0.012	0.017
6	<i>Urodacus varians</i> PC03	0.182	0.172	0.178	0.180	0.186		0.017	0.014
7	<i>Lychas annulatus</i> clade B PC04	0.028	0.102	0.028	0.004	0.076	0.176		0.018
8	<i>Urodacus</i> sp Telfer PC05	0.198	0.172	0.198	0.196	0.184	0.110	0.192	
9	<i>Lychas annulatus</i> clade A PC06	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
10	<i>Urodacus yaschenkoki</i> PC07	0.190	0.182	0.186	0.194	0.188	0.100	0.194	0.094
11	<i>Urodacus yaschenkoki</i> PC08	0.190	0.182	0.186	0.194	0.188	0.100	0.194	0.094
12	<i>Lychas annulatus</i> clade B NN01	0.014	0.108	0.014	0.030	0.086	0.188	0.030	0.208
13	<i>Lychas annulatus</i> clade A NN03	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
14	<i>Lychas annulatus</i> clade B NN04	0.010	0.104	0.010	0.026	0.078	0.184	0.026	0.200
15	<i>Lychas annulatus</i> NN05 clade A	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
16	<i>Lychas annulatus</i> clade A NN06	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
17	<i>Lychas annulatus</i> clade A NN07	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
18	<i>Lychas annulatus</i> clade A NN08	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
19	<i>Lychas annulatus</i> clade B NN09	0.008	0.094	0.004	0.024	0.080	0.178	0.028	0.198
20	<i>Lychas annulatus</i> clade ANN10	0.072	0.104	0.076	0.076	0.000	0.186	0.076	0.184
21	EF122605.2 <i>Centruroides vittatus</i>	0.162	0.176	0.166	0.160	0.184	0.192	0.160	0.206
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.186	0.176	0.190	0.186	0.170	0.128	0.186	0.086
23	KT446990. <i>Brachistosternus paposo</i>	0.184	0.174	0.186	0.178	0.182	0.158	0.182	0.148
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.190	0.184	0.190	0.188	0.174	0.156	0.192	0.156
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.170	0.166	0.166	0.172	0.182	0.140	0.176	0.162
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.194	0.192	0.196	0.190	0.202	0.150	0.190	0.154
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.180	0.170	0.176	0.172	0.182	0.140	0.172	0.130
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.174	0.160	0.178	0.174	0.178	0.154	0.178	0.142
29	KX517230.1 <i>Brachistosternus paposo</i>	0.184	0.174	0.186	0.178	0.182	0.158	0.182	0.148
30	KX517229.1 <i>Brachistosternus paposo</i>	0.184	0.174	0.186	0.178	0.182	0.158	0.182	0.148
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.192	0.174	0.188	0.194	0.188	0.158	0.194	0.162
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.196	0.186	0.192	0.198	0.186	0.158	0.198	0.154
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.186	0.172	0.192	0.186	0.178	0.152	0.186	0.132
34	AY156581.1 <i>Pandinus dictator</i>	0.204	0.200	0.202	0.200	0.198	0.138	0.204	0.148
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.200	0.192	0.200	0.198	0.188	0.162	0.198	0.132
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.192	0.176	0.198	0.186	0.192	0.164	0.182	0.144

		1	2	3	4	5	6	7	8
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.168	0.178	0.168	0.174	0.176	0.154	0.174	0.158
38	KT446946.1 <i>Brachistosternus chango</i>	0.196	0.174	0.198	0.192	0.186	0.148	0.192	0.152
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.198	0.190	0.200	0.194	0.198	0.180	0.198	0.168
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.190	0.184	0.188	0.188	0.196	0.160	0.188	0.168
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.214	0.192	0.216	0.212	0.190	0.158	0.208	0.144
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.196	0.202	0.204	0.202	0.190	0.168	0.202	0.148
43	KX517244.1 <i>Brachistosternus paposo</i>	0.186	0.178	0.192	0.180	0.180	0.158	0.180	0.152
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.200	0.184	0.202	0.206	0.198	0.166	0.206	0.160
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.178	0.184	0.182	0.176	0.192	0.166	0.176	0.162
46	KT446986.1 <i>Brachistosternus negrei</i>	0.194	0.180	0.198	0.196	0.184	0.160	0.196	0.158
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.162	0.172	0.162	0.168	0.168	0.152	0.168	0.154
48	JX909544.1 <i>Paruroctonus boreus</i> SKY42/AMNH	0.178	0.180	0.178	0.178	0.180	0.158	0.182	0.160
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.194	0.190	0.202	0.190	0.194	0.144	0.190	0.152
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.184	0.178	0.184	0.194	0.182	0.142	0.190	0.136
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.190	0.182	0.190	0.186	0.182	0.146	0.186	0.150
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.218	0.198	0.214	0.216	0.214	0.168	0.220	0.172
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.180	0.184	0.186	0.182	0.186	0.174	0.182	0.164
54	KT188365.1 <i>Scorpio palmatus</i>	0.198	0.180	0.196	0.200	0.202	0.154	0.200	0.168
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.196	0.186	0.192	0.186	0.206	0.152	0.190	0.162
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.192	0.182	0.194	0.186	0.182	0.142	0.190	0.156
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.220	0.196	0.222	0.222	0.208	0.180	0.226	0.166
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.214	0.192	0.212	0.212	0.212	0.166	0.208	0.176
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.196	0.178	0.194	0.198	0.200	0.154	0.198	0.170
60	EF122607.2 <i>Centruroides vittatus</i>	0.162	0.176	0.166	0.160	0.184	0.192	0.160	0.206
61	EF122608.2 <i>Centruroides vittatus</i>	0.162	0.172	0.166	0.160	0.190	0.196	0.160	0.210
62	EF122612.2 <i>Centruroides vittatus</i>	0.160	0.174	0.164	0.158	0.186	0.194	0.158	0.204
63	EU381064.1 <i>Centruroides vittatus</i>	0.160	0.174	0.164	0.158	0.186	0.194	0.158	0.204
64	EU404114.1 <i>Centruroides vittatus</i>	0.164	0.176	0.166	0.160	0.182	0.198	0.160	0.212
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.158	0.152	0.158	0.156	0.162	0.202	0.156	0.206
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.180	0.172	0.184	0.168	0.184	0.202	0.164	0.198
67	JN018153.1 <i>Lychas mucronatus</i>	0.138	0.138	0.142	0.142	0.126	0.202	0.142	0.194
68	JN018154.1 <i>Parabuthus laevisfrons</i>	0.152	0.160	0.152	0.156	0.154	0.200	0.160	0.200
69	JN018210.1 <i>Lychas mucronatus</i>	0.150	0.142	0.150	0.148	0.150	0.196	0.148	0.202
70	JN018211.1 <i>Lychas mucronatus</i>	0.160	0.150	0.152	0.156	0.160	0.206	0.160	0.210
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.154	0.178	0.162	0.160	0.168	0.212	0.164	0.218
72	KT716037.1 <i>Lychas tricarinatus</i>	0.152	0.140	0.148	0.158	0.140	0.198	0.158	0.198

		1	2	3	4	5	6	7	8
73	KX648425.1 <i>Hottentotta minax</i>	0.166	0.176	0.164	0.166	0.160	0.210	0.164	0.202
74	KX648429.1 <i>Compsobuthus weneri</i>	0.166	0.176	0.164	0.166	0.160	0.210	0.164	0.202
75	KY982184.1 <i>Centruroides schmidt</i>	0.156	0.162	0.156	0.162	0.156	0.190	0.162	0.192
76	KY982185.1 <i>Centruroides vittatus</i>	0.164	0.170	0.166	0.160	0.178	0.194	0.160	0.210
77	KY982187.1 <i>Heteroctenus abudi</i>	0.160	0.176	0.164	0.158	0.140	0.192	0.162	0.194
78	KY982188.1 <i>Heteroctenus abudi</i>	0.158	0.178	0.162	0.160	0.142	0.198	0.164	0.200
79	KY982192.1 <i>Heteroctenus junceus</i>	0.176	0.188	0.178	0.172	0.182	0.188	0.172	0.204
80	KY982193.1 <i>Heteroctenus junceus</i>	0.174	0.186	0.176	0.170	0.180	0.188	0.170	0.204
81	KY982194.1 <i>Heteroctenus junceus</i>	0.160	0.182	0.164	0.162	0.170	0.184	0.162	0.200
82	KY982199.1 <i>Heteroctenus junceus</i>	0.162	0.180	0.166	0.164	0.172	0.182	0.164	0.200
83	KY982273.1 <i>Zabius fuscus</i>	0.162	0.178	0.168	0.162	0.152	0.218	0.162	0.234
84	MF422313.1 <i>Isometrus</i> sp.	0.126	0.142	0.128	0.130	0.136	0.174	0.126	0.196
85	MF422319.1 <i>Lychas tricarinatus</i>	0.150	0.134	0.146	0.156	0.138	0.190	0.156	0.194
86	MF422320.1 <i>Lychas tricarinatus</i>	0.150	0.132	0.146	0.156	0.138	0.188	0.156	0.194
87	MF422321.1 <i>Lychas tricarinatus</i>	0.146	0.134	0.142	0.152	0.134	0.190	0.152	0.194
88	MF422322.1 <i>Lychas tricarinatus</i>	0.150	0.132	0.146	0.156	0.138	0.188	0.156	0.194
89	MF422326.1 <i>Lychas tricarinatus</i>	0.150	0.138	0.146	0.144	0.150	0.198	0.144	0.208
90	MF422327.1 <i>Lychas tricarinatus</i>	0.148	0.144	0.144	0.146	0.154	0.186	0.142	0.196
91	MF422328.1 <i>Lychas tricarinatus</i>	0.154	0.140	0.152	0.146	0.156	0.198	0.146	0.210
92	MF422329.1 <i>Lychas tricarinatus</i>	0.148	0.146	0.144	0.146	0.154	0.188	0.142	0.198
93	MF422330.1 <i>Lychas tricarinatus</i>	0.148	0.144	0.144	0.146	0.154	0.186	0.142	0.196
94	MK479161.1 <i>Centruroides arctimanus</i>	0.172	0.176	0.172	0.174	0.168	0.194	0.170	0.204
95	MK479165.1 <i>Centruroides barbudensis</i>	0.166	0.164	0.166	0.172	0.180	0.198	0.172	0.198
96	MK479171.1 <i>Centruroides exilimanus</i>	0.166	0.172	0.164	0.166	0.178	0.188	0.166	0.212
97	MK479180.1 <i>Centruroides insulanus</i>	0.160	0.160	0.164	0.166	0.162	0.184	0.170	0.190
98	MK479188.1 <i>Centruroides morenoi</i>	0.172	0.174	0.174	0.174	0.168	0.200	0.174	0.188
99	MK479196.1 <i>Centruroides platnicki</i>	0.160	0.156	0.162	0.162	0.156	0.182	0.158	0.202
100	MK479202.1 <i>Centruroides simplex</i>	0.150	0.154	0.156	0.156	0.160	0.190	0.156	0.178
101	MK479204.1 <i>Centruroides taino</i>	0.150	0.156	0.150	0.152	0.160	0.180	0.156	0.190
102	MK479207.1 <i>Centruroides testaceus</i>	0.150	0.168	0.148	0.152	0.156	0.180	0.152	0.186
103	MK479210.1 <i>Centruroides vittatus</i>	0.166	0.178	0.168	0.162	0.184	0.200	0.162	0.214
104	NC 037222.1 <i>Centruroides vittatus</i>	0.166	0.178	0.168	0.162	0.184	0.200	0.162	0.214
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.196	0.176	0.194	0.200	0.186	0.142	0.204	0.142
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.200	0.218	0.200	0.196	0.196	0.174	0.196	0.176
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.208	0.192	0.206	0.212	0.190	0.170	0.216	0.170
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.190	0.182	0.190	0.186	0.182	0.146	0.186	0.150

		9	10	11	12	13	14	15	16
1	PP07	0.012	0.018	0.018	0.005	0.012	0.004	0.012	0.012
2	PP08	0.014	0.017	0.017	0.014	0.014	0.014	0.014	0.014
3	PP11	0.012	0.017	0.017	0.005	0.012	0.004	0.012	0.012
4	<i>Lychas annulatus</i> clade B PC01	0.012	0.018	0.018	0.008	0.012	0.007	0.012	0.012
5	<i>Lychas annulatus</i> clade A PC02	0.000	0.017	0.017	0.013	0.000	0.012	0.000	0.000
6	<i>Urodacus varians</i> PC03	0.017	0.013	0.013	0.017	0.017	0.017	0.017	0.017
7	<i>Lychas annulatus</i> clade B PC04	0.012	0.018	0.018	0.008	0.012	0.007	0.012	0.012
8	<i>Urodacus</i> sp Telfer PC05	0.017	0.013	0.013	0.018	0.017	0.018	0.017	0.017
9	<i>Lychas annulatus</i> clade A PC06		0.017	0.017	0.013	0.000	0.012	0.000	0.000
10	<i>Urodacus yaschenkoki</i> PC07	0.188		0.000	0.018	0.017	0.017	0.017	0.017
11	<i>Urodacus yaschenkoki</i> PC08	0.188	0.000		0.018	0.017	0.017	0.017	0.017
12	<i>Lychas annulatus</i> clade B NN01	0.086	0.196	0.196		0.013	0.004	0.013	0.013
13	<i>Lychas annulatus</i> clade A NN03	0.000	0.188	0.188	0.086		0.012	0.000	0.000
14	<i>Lychas annulatus</i> clade B NN04	0.078	0.188	0.188	0.008	0.078		0.012	0.012
15	<i>Lychas annulatus</i> NN05 clade A	0.000	0.188	0.188	0.086	0.000	0.078		0.000
16	<i>Lychas annulatus</i> clade A NN06	0.000	0.188	0.188	0.086	0.000	0.078	0.000	
17	<i>Lychas annulatus</i> clade A NN07	0.000	0.188	0.188	0.086	0.000	0.078	0.000	0.000
18	<i>Lychas annulatus</i> clade A NN08	0.000	0.188	0.188	0.086	0.000	0.078	0.000	0.000
19	<i>Lychas annulatus</i> clade B NN09	0.080	0.190	0.190	0.014	0.080	0.010	0.080	0.080
20	<i>Lychas annulatus</i> clade ANN10	0.000	0.188	0.188	0.086	0.000	0.078	0.000	0.000
21	EF122605.2 <i>Centruroides vittatus</i>	0.184	0.208	0.208	0.166	0.184	0.166	0.184	0.184
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.170	0.108	0.108	0.200	0.170	0.192	0.170	0.170
23	KT446990. <i>Brachistosternus paposo</i>	0.182	0.138	0.138	0.192	0.182	0.184	0.182	0.182
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.174	0.136	0.136	0.198	0.174	0.190	0.174	0.174
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.182	0.130	0.130	0.180	0.182	0.176	0.182	0.182
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.202	0.140	0.140	0.200	0.202	0.192	0.202	0.202
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.182	0.132	0.132	0.184	0.182	0.176	0.182	0.182
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.178	0.144	0.144	0.180	0.178	0.180	0.178	0.178
29	KX517230.1 <i>Brachistosternus paposo</i>	0.182	0.138	0.138	0.192	0.182	0.184	0.182	0.182
30	KX517229.1 <i>Brachistosternus paposo</i>	0.182	0.138	0.138	0.192	0.182	0.184	0.182	0.182
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.188	0.146	0.146	0.196	0.188	0.192	0.188	0.188
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.186	0.144	0.144	0.204	0.186	0.200	0.186	0.186
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.178	0.142	0.142	0.196	0.178	0.188	0.178	0.178
34	AY156581.1 <i>Pandinus dictator</i>	0.198	0.126	0.126	0.214	0.198	0.206	0.198	0.198
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.188	0.138	0.138	0.202	0.188	0.198	0.188	0.188
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.192	0.146	0.146	0.196	0.192	0.196	0.192	0.192

		9	10	11	12	13	14	15	16
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.176	0.136	0.136	0.176	0.176	0.172	0.176	0.176
38	KT446946.1 <i>Brachistosternus chango</i>	0.186	0.150	0.150	0.206	0.186	0.202	0.186	0.186
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.198	0.162	0.162	0.212	0.198	0.204	0.198	0.198
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.196	0.148	0.148	0.194	0.196	0.190	0.196	0.196
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.190	0.138	0.138	0.222	0.190	0.216	0.190	0.190
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.190	0.154	0.154	0.206	0.190	0.198	0.190	0.190
43	KX517244.1 <i>Brachistosternus paposo</i>	0.180	0.144	0.144	0.190	0.180	0.186	0.180	0.180
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.198	0.156	0.156	0.208	0.198	0.200	0.198	0.198
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.192	0.150	0.150	0.182	0.192	0.174	0.192	0.192
46	KT446986.1 <i>Brachistosternus negrei</i>	0.184	0.154	0.154	0.206	0.184	0.202	0.184	0.184
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.168	0.144	0.144	0.170	0.168	0.166	0.168	0.168
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.180	0.154	0.154	0.190	0.180	0.184	0.180	0.180
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.194	0.156	0.156	0.208	0.194	0.204	0.194	0.194
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.182	0.150	0.150	0.194	0.182	0.186	0.182	0.182
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.182	0.142	0.142	0.200	0.182	0.196	0.182	0.182
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.214	0.152	0.152	0.226	0.214	0.218	0.214	0.214
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.186	0.152	0.152	0.188	0.186	0.180	0.186	0.186
54	KT188365.1 <i>Scorpio palmatus</i>	0.202	0.154	0.154	0.202	0.202	0.194	0.202	0.202
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.206	0.140	0.140	0.206	0.206	0.202	0.206	0.206
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.182	0.144	0.144	0.198	0.182	0.198	0.182	0.182
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.208	0.170	0.170	0.230	0.208	0.226	0.208	0.208
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.212	0.160	0.160	0.214	0.212	0.212	0.212	0.212
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.200	0.152	0.152	0.200	0.200	0.192	0.200	0.200
60	EF122607.2 <i>Centruroides vittatus</i>	0.184	0.208	0.208	0.166	0.184	0.166	0.184	0.184
61	EF122608.2 <i>Centruroides vittatus</i>	0.190	0.210	0.210	0.166	0.190	0.166	0.190	0.190
62	EF122612.2 <i>Centruroides vittatus</i>	0.186	0.206	0.206	0.164	0.186	0.164	0.186	0.186
63	EU381064.1 <i>Centruroides vittatus</i>	0.186	0.206	0.206	0.164	0.186	0.164	0.186	0.186
64	EU404114.1 <i>Centruroides vittatus</i>	0.182	0.200	0.200	0.164	0.182	0.164	0.182	0.182
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.162	0.208	0.208	0.172	0.162	0.168	0.162	0.162
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.184	0.202	0.202	0.182	0.184	0.182	0.184	0.184
67	JN018153.1 <i>Lychas mucronatus</i>	0.126	0.208	0.208	0.150	0.126	0.144	0.126	0.126
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.154	0.196	0.196	0.162	0.154	0.154	0.154	0.154
69	JN018210.1 <i>Lychas mucronatus</i>	0.150	0.200	0.200	0.156	0.150	0.156	0.150	0.150
70	JN018211.1 <i>Lychas mucronatus</i>	0.160	0.212	0.212	0.154	0.160	0.158	0.160	0.160
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.168	0.202	0.202	0.164	0.168	0.160	0.168	0.168
72	KT716037.1 <i>Lychas tricarinatus</i>	0.140	0.196	0.196	0.162	0.140	0.154	0.140	0.140

		9	10	11	12	13	14	15	16
73	KX648425.1 <i>Hottentotta minax</i>	0.160	0.208	0.208	0.166	0.160	0.166	0.160	0.160
74	KX648429.1 <i>Compsobuthus weneri</i>	0.160	0.208	0.208	0.166	0.160	0.166	0.160	0.160
75	KY982184.1 <i>Centruroides schmidt</i>	0.156	0.190	0.190	0.162	0.156	0.162	0.156	0.156
76	KY982185.1 <i>Centruroides vittatus</i>	0.178	0.196	0.196	0.166	0.178	0.166	0.178	0.178
77	KY982187.1 <i>Heteroctenus abudi</i>	0.140	0.202	0.202	0.170	0.140	0.164	0.140	0.140
78	KY982188.1 <i>Heteroctenus abudi</i>	0.142	0.204	0.204	0.168	0.142	0.162	0.142	0.142
79	KY982192.1 <i>Heteroctenus junceus</i>	0.182	0.196	0.196	0.182	0.182	0.180	0.182	0.182
80	KY982193.1 <i>Heteroctenus junceus</i>	0.180	0.196	0.196	0.180	0.180	0.178	0.180	0.180
81	KY982194.1 <i>Heteroctenus junceus</i>	0.170	0.194	0.194	0.168	0.170	0.166	0.170	0.170
82	KY982199.1 <i>Heteroctenus junceus</i>	0.172	0.184	0.184	0.166	0.172	0.160	0.172	0.172
83	KY982273.1 <i>Zabius fuscus</i>	0.152	0.234	0.234	0.174	0.152	0.170	0.152	0.152
84	MF422313.1 <i>Isometrus</i> sp.	0.136	0.196	0.196	0.132	0.136	0.130	0.136	0.136
85	MF422319.1 <i>Lychas tricarinatus</i>	0.138	0.200	0.200	0.160	0.138	0.152	0.138	0.138
86	MF422320.1 <i>Lychas tricarinatus</i>	0.138	0.198	0.198	0.160	0.138	0.152	0.138	0.138
87	MF422321.1 <i>Lychas tricarinatus</i>	0.134	0.196	0.196	0.156	0.134	0.148	0.134	0.134
88	MF422322.1 <i>Lychas tricarinatus</i>	0.138	0.198	0.198	0.160	0.138	0.152	0.138	0.138
89	MF422326.1 <i>Lychas tricarinatus</i>	0.150	0.210	0.210	0.160	0.150	0.156	0.150	0.150
90	MF422327.1 <i>Lychas tricarinatus</i>	0.154	0.202	0.202	0.154	0.154	0.150	0.154	0.154
91	MF422328.1 <i>Lychas tricarinatus</i>	0.156	0.212	0.212	0.166	0.156	0.162	0.156	0.156
92	MF422329.1 <i>Lychas tricarinatus</i>	0.154	0.200	0.200	0.154	0.154	0.150	0.154	0.154
93	MF422330.1 <i>Lychas tricarinatus</i>	0.154	0.202	0.202	0.154	0.154	0.150	0.154	0.154
94	MK479161.1 <i>Centruroides arctimanus</i>	0.168	0.204	0.204	0.176	0.168	0.174	0.168	0.168
95	MK479165.1 <i>Centruroides barbudensis</i>	0.180	0.202	0.202	0.168	0.180	0.170	0.180	0.180
96	MK479171.1 <i>Centruroides exilimanus</i>	0.178	0.206	0.206	0.172	0.178	0.172	0.178	0.178
97	MK479180.1 <i>Centruroides insulanus</i>	0.162	0.178	0.178	0.172	0.162	0.166	0.162	0.162
98	MK479188.1 <i>Centruroides morenoi</i>	0.168	0.196	0.196	0.176	0.168	0.178	0.168	0.168
99	MK479196.1 <i>Centruroides platnicki</i>	0.156	0.200	0.200	0.166	0.156	0.164	0.156	0.156
100	MK479202.1 <i>Centruroides simplex</i>	0.160	0.184	0.184	0.156	0.160	0.152	0.160	0.160
101	MK479204.1 <i>Centruroides taino</i>	0.160	0.188	0.188	0.162	0.160	0.156	0.160	0.160
102	MK479207.1 <i>Centruroides testaceus</i>	0.156	0.182	0.182	0.152	0.156	0.148	0.156	0.156
103	MK479210.1 <i>Centruroides vittatus</i>	0.184	0.202	0.202	0.166	0.184	0.166	0.184	0.184
104	NC 037222.1 <i>Centruroides vittatus</i>	0.184	0.202	0.202	0.166	0.184	0.166	0.184	0.184
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.186	0.154	0.154	0.208	0.186	0.204	0.186	0.186
106	JN018163.1 <i>Chaerilus juliettea</i> voucher MNHN-JAB32	0.196	0.172	0.172	0.206	0.196	0.198	0.196	0.196
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.190	0.186	0.186	0.218	0.190	0.214	0.190	0.190
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.182	0.142	0.142	0.200	0.182	0.196	0.182	0.182

		17	18	19	20	21	22	23	24
1	PP07	0.012	0.012	0.004	0.012	0.016	0.017	0.017	0.018
2	PP08	0.014	0.014	0.013	0.014	0.017	0.017	0.017	0.017
3	PP11	0.012	0.012	0.003	0.012	0.017	0.018	0.017	0.018
4	<i>Lychas annulatus</i> clade B PC01	0.012	0.012	0.007	0.012	0.016	0.017	0.017	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.000	0.000	0.012	0.000	0.017	0.017	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.017	0.017	0.017	0.017	0.018	0.015	0.016	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.012	0.012	0.007	0.012	0.016	0.017	0.017	0.018
8	<i>Urodacus</i> sp Telfer PC05	0.017	0.017	0.018	0.017	0.018	0.013	0.016	0.016
9	<i>Lychas annulatus</i> clade A PC06	0.000	0.000	0.012	0.000	0.017	0.017	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.017	0.017	0.018	0.017	0.018	0.014	0.015	0.015
11	<i>Urodacus yaschenkoki</i> PC08	0.017	0.017	0.018	0.017	0.018	0.014	0.015	0.015
12	<i>Lychas annulatus</i> clade B NN01	0.013	0.013	0.005	0.013	0.017	0.018	0.018	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.000	0.000	0.012	0.000	0.017	0.017	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.012	0.012	0.004	0.012	0.017	0.018	0.017	0.018
15	<i>Lychas annulatus</i> NN05 clade A	0.000	0.000	0.012	0.000	0.017	0.017	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.000	0.000	0.012	0.000	0.017	0.017	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07		0.000	0.012	0.000	0.017	0.017	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.000		0.012	0.000	0.017	0.017	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.080	0.080		0.012	0.017	0.018	0.017	0.018
20	<i>Lychas annulatus</i> clade ANN10	0.000	0.000	0.080		0.017	0.017	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.184	0.184	0.168	0.184		0.018	0.017	0.018
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.170	0.170	0.194	0.170	0.218		0.016	0.016
23	KT446990. <i>Brachistosternus paposo</i>	0.182	0.182	0.186	0.182	0.178	0.144		0.010
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.174	0.174	0.194	0.174	0.192	0.146	0.056	
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.182	0.182	0.170	0.182	0.188	0.150	0.100	0.100
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.202	0.202	0.196	0.202	0.194	0.154	0.144	0.158
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.182	0.182	0.176	0.182	0.164	0.152	0.138	0.148
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.178	0.178	0.178	0.178	0.196	0.132	0.140	0.152
29	KX517230.1 <i>Brachistosternus paposo</i>	0.182	0.182	0.186	0.182	0.178	0.144	0.000	0.056
30	KX517229.1 <i>Brachistosternus paposo</i>	0.182	0.182	0.186	0.182	0.178	0.144	0.000	0.056
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.188	0.188	0.192	0.188	0.208	0.146	0.100	0.114
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.186	0.186	0.196	0.186	0.214	0.148	0.108	0.116
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.178	0.178	0.192	0.178	0.200	0.128	0.144	0.158
34	AY156581.1 <i>Pandinus dictator</i>	0.198	0.198	0.204	0.198	0.180	0.140	0.154	0.156
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.188	0.188	0.204	0.188	0.198	0.138	0.138	0.146
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.192	0.192	0.198	0.192	0.186	0.142	0.030	0.062

		17	18	19	20	21	22	23	24
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.176	0.176	0.172	0.176	0.184	0.158	0.098	0.116
38	KT446946.1 <i>Brachistosternus chango</i>	0.186	0.186	0.202	0.186	0.192	0.148	0.098	0.108
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.198	0.198	0.202	0.198	0.198	0.166	0.160	0.160
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.196	0.196	0.192	0.196	0.194	0.162	0.114	0.106
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.190	0.190	0.218	0.190	0.186	0.144	0.154	0.156
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.190	0.190	0.204	0.190	0.186	0.144	0.128	0.146
43	KX517244.1 <i>Brachistosternus paposo</i>	0.180	0.180	0.192	0.180	0.178	0.150	0.026	0.052
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.198	0.198	0.202	0.198	0.198	0.154	0.102	0.108
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.192	0.192	0.182	0.192	0.178	0.150	0.052	0.052
46	KT446986.1 <i>Brachistosternus negrei</i>	0.184	0.184	0.202	0.184	0.198	0.144	0.114	0.102
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.168	0.168	0.166	0.168	0.190	0.154	0.100	0.122
48	JX909544.1 <i>Paruroctonus boreus</i> SKY42/AMNH	0.180	0.180	0.182	0.180	0.196	0.162	0.154	0.160
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.194	0.194	0.202	0.194	0.192	0.128	0.116	0.128
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.182	0.182	0.184	0.182	0.194	0.144	0.168	0.168
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.182	0.182	0.192	0.182	0.186	0.132	0.154	0.170
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.214	0.214	0.218	0.214	0.222	0.154	0.110	0.108
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.186	0.186	0.186	0.186	0.190	0.154	0.050	0.050
54	KT188365.1 <i>Scorpio palmatus</i>	0.202	0.202	0.200	0.202	0.188	0.164	0.172	0.188
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.206	0.206	0.196	0.206	0.188	0.154	0.142	0.162
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.182	0.182	0.196	0.182	0.172	0.156	0.156	0.162
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.208	0.208	0.224	0.208	0.194	0.170	0.148	0.172
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.212	0.212	0.216	0.212	0.194	0.172	0.160	0.166
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.200	0.200	0.198	0.200	0.188	0.162	0.170	0.186
60	EF122607.2 <i>Centruroides vittatus</i>	0.184	0.184	0.168	0.184	0.000	0.218	0.178	0.192
61	EF122608.2 <i>Centruroides vittatus</i>	0.190	0.190	0.168	0.190	0.016	0.224	0.176	0.190
62	EF122612.2 <i>Centruroides vittatus</i>	0.186	0.186	0.166	0.186	0.004	0.216	0.178	0.192
63	EU381064.1 <i>Centruroides vittatus</i>	0.186	0.186	0.166	0.186	0.002	0.216	0.178	0.192
64	EU404114.1 <i>Centruroides vittatus</i>	0.182	0.182	0.168	0.182	0.030	0.210	0.178	0.182
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.162	0.162	0.162	0.162	0.170	0.218	0.210	0.208
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.184	0.184	0.184	0.184	0.160	0.212	0.212	0.214
67	JN018153.1 <i>Lychas mucronatus</i>	0.126	0.126	0.146	0.126	0.172	0.208	0.196	0.190
68	JN018154.1 <i>Parabuthus laevisfrons</i>	0.154	0.154	0.152	0.154	0.172	0.204	0.182	0.182
69	JN018210.1 <i>Lychas mucronatus</i>	0.150	0.150	0.154	0.150	0.164	0.214	0.180	0.188
70	JN018211.1 <i>Lychas mucronatus</i>	0.160	0.160	0.152	0.160	0.194	0.216	0.198	0.202
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.168	0.168	0.162	0.168	0.158	0.206	0.202	0.206
72	KT716037.1 <i>Lychas tricarinatus</i>	0.140	0.140	0.152	0.140	0.168	0.202	0.200	0.196

		17	18	19	20	21	22	23	24
73	KX648425.1 <i>Hottentotta minax</i>	0.160	0.160	0.168	0.160	0.188	0.208	0.214	0.206
74	KX648429.1 <i>Compsobuthus weneri</i>	0.160	0.160	0.168	0.160	0.188	0.208	0.214	0.206
75	KY982184.1 <i>Centruroides schmidt</i>	0.156	0.156	0.160	0.156	0.118	0.192	0.180	0.174
76	KY982185.1 <i>Centruroides vittatus</i>	0.178	0.178	0.168	0.178	0.026	0.212	0.178	0.182
77	KY982187.1 <i>Heteroctenus abudi</i>	0.140	0.140	0.168	0.140	0.148	0.192	0.184	0.186
78	KY982188.1 <i>Heteroctenus abudi</i>	0.142	0.142	0.166	0.142	0.138	0.198	0.186	0.192
79	KY982192.1 <i>Heteroctenus junceus</i>	0.182	0.182	0.178	0.182	0.126	0.198	0.198	0.196
80	KY982193.1 <i>Heteroctenus junceus</i>	0.180	0.180	0.176	0.180	0.126	0.198	0.198	0.196
81	KY982194.1 <i>Heteroctenus junceus</i>	0.170	0.170	0.164	0.170	0.122	0.198	0.200	0.192
82	KY982199.1 <i>Heteroctenus junceus</i>	0.172	0.172	0.166	0.172	0.114	0.194	0.184	0.188
83	KY982273.1 <i>Zabius fuscus</i>	0.152	0.152	0.168	0.152	0.166	0.216	0.200	0.200
84	MF422313.1 <i>Isometrus</i> sp.	0.136	0.136	0.124	0.136	0.178	0.212	0.210	0.214
85	MF422319.1 <i>Lychas tricarinatus</i>	0.138	0.138	0.146	0.138	0.166	0.210	0.200	0.192
86	MF422320.1 <i>Lychas tricarinatus</i>	0.138	0.138	0.146	0.138	0.168	0.210	0.198	0.194
87	MF422321.1 <i>Lychas tricarinatus</i>	0.134	0.134	0.146	0.134	0.164	0.206	0.194	0.190
88	MF422322.1 <i>Lychas tricarinatus</i>	0.138	0.138	0.146	0.138	0.168	0.210	0.198	0.194
89	MF422326.1 <i>Lychas tricarinatus</i>	0.150	0.150	0.146	0.150	0.152	0.218	0.202	0.202
90	MF422327.1 <i>Lychas tricarinatus</i>	0.154	0.154	0.148	0.154	0.138	0.214	0.200	0.208
91	MF422328.1 <i>Lychas tricarinatus</i>	0.156	0.156	0.156	0.156	0.144	0.212	0.204	0.206
92	MF422329.1 <i>Lychas tricarinatus</i>	0.154	0.154	0.148	0.154	0.140	0.214	0.202	0.210
93	MF422330.1 <i>Lychas tricarinatus</i>	0.154	0.154	0.148	0.154	0.138	0.214	0.200	0.208
94	MK479161.1 <i>Centruroides arctimanus</i>	0.168	0.168	0.172	0.168	0.140	0.194	0.192	0.182
95	MK479165.1 <i>Centruroides barbudensis</i>	0.180	0.180	0.166	0.180	0.128	0.216	0.190	0.192
96	MK479171.1 <i>Centruroides exilimanus</i>	0.178	0.178	0.166	0.178	0.118	0.210	0.190	0.188
97	MK479180.1 <i>Centruroides insulanus</i>	0.162	0.162	0.168	0.162	0.122	0.182	0.190	0.174
98	MK479188.1 <i>Centruroides morenoi</i>	0.168	0.168	0.176	0.168	0.102	0.196	0.186	0.186
99	MK479196.1 <i>Centruroides platnicki</i>	0.156	0.156	0.166	0.156	0.120	0.204	0.170	0.182
100	MK479202.1 <i>Centruroides simplex</i>	0.160	0.160	0.158	0.160	0.100	0.184	0.172	0.170
101	MK479204.1 <i>Centruroides taino</i>	0.160	0.160	0.154	0.160	0.130	0.200	0.184	0.184
102	MK479207.1 <i>Centruroides testaceus</i>	0.156	0.156	0.150	0.156	0.108	0.186	0.168	0.170
103	MK479210.1 <i>Centruroides vittatus</i>	0.184	0.184	0.170	0.184	0.032	0.212	0.180	0.184
104	NC 037222.1 <i>Centruroides vittatus</i>	0.184	0.184	0.170	0.184	0.032	0.212	0.180	0.184
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.186	0.186	0.198	0.186	0.208	0.148	0.156	0.152
106	JN018163.1 <i>Chaerilus juliettea</i> voucher MNHN-JAB32	0.196	0.196	0.198	0.196	0.198	0.188	0.180	0.182
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.190	0.190	0.206	0.190	0.228	0.158	0.172	0.152
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.182	0.182	0.192	0.182	0.186	0.132	0.154	0.170

		25	26	27	28	29	30	31	32
1	PP07	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
2	PP08	0.017	0.018	0.017	0.016	0.017	0.017	0.017	0.017
3	PP11	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.018
4	<i>Lychas annulatus</i> clade B PC01	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
5	<i>Lychas annulatus</i> clade A PC02	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
8	<i>Urodacus</i> sp Telfer PC05	0.016	0.016	0.015	0.016	0.016	0.016	0.016	0.016
9	<i>Lychas annulatus</i> clade A PC06	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.015	0.016	0.015	0.016	0.015	0.015	0.016	0.016
11	<i>Urodacus yaschenkoki</i> PC08	0.015	0.016	0.015	0.016	0.015	0.015	0.016	0.016
12	<i>Lychas annulatus</i> clade B NN01	0.017	0.018	0.017	0.017	0.018	0.018	0.018	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
15	<i>Lychas annulatus</i> NN05 clade A	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
20	<i>Lychas annulatus</i> clade ANN10	0.017	0.018	0.017	0.017	0.017	0.017	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.016	0.016	0.016	0.015	0.016	0.016	0.016	0.016
23	KT446990. <i>Brachistosternus paposo</i>	0.013	0.016	0.015	0.016	0.000	0.000	0.013	0.014
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.013	0.016	0.016	0.016	0.010	0.010	0.014	0.014
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>		0.016	0.015	0.015	0.013	0.013	0.014	0.013
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.148		0.014	0.015	0.016	0.016	0.017	0.017
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.128	0.116		0.014	0.015	0.015	0.015	0.016
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.124	0.122	0.118		0.016	0.016	0.016	0.016
29	KX517230.1 <i>Brachistosternus paposo</i>	0.100	0.144	0.138	0.140		0.000	0.013	0.014
30	KX517229.1 <i>Brachistosternus paposo</i>	0.100	0.144	0.138	0.140	0.000		0.013	0.014
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.110	0.168	0.132	0.146	0.100	0.100		0.010
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.100	0.172	0.144	0.160	0.108	0.108	0.056	
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.140	0.122	0.122	0.076	0.144	0.144	0.144	0.154
34	AY156581.1 <i>Pandinus dictator</i>	0.156	0.140	0.120	0.148	0.154	0.154	0.162	0.156
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.154	0.102	0.110	0.106	0.138	0.138	0.138	0.150
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.110	0.148	0.150	0.152	0.030	0.030	0.108	0.118

		25	26	27	28	29	30	31	32
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.092	0.144	0.132	0.132	0.098	0.098	0.096	0.106
38	KT446946.1 <i>Brachistosternus chango</i>	0.110	0.168	0.128	0.132	0.098	0.098	0.064	0.074
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.168	0.176	0.164	0.174	0.160	0.160	0.160	0.168
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.066	0.150	0.130	0.146	0.114	0.114	0.106	0.104
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.170	0.148	0.134	0.160	0.154	0.154	0.174	0.182
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.152	0.124	0.128	0.140	0.128	0.128	0.160	0.172
43	KX517244.1 <i>Brachistosternus paposo</i>	0.108	0.144	0.144	0.146	0.026	0.026	0.112	0.126
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.120	0.166	0.146	0.168	0.102	0.102	0.098	0.094
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.104	0.146	0.142	0.144	0.052	0.052	0.106	0.122
46	KT446986.1 <i>Brachistosternus negrei</i>	0.120	0.168	0.140	0.150	0.114	0.114	0.066	0.076
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.086	0.148	0.136	0.124	0.100	0.100	0.094	0.102
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.148	0.164	0.142	0.146	0.154	0.154	0.148	0.152
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.122	0.156	0.146	0.150	0.116	0.116	0.134	0.134
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.144	0.140	0.104	0.124	0.168	0.168	0.150	0.144
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.144	0.168	0.150	0.132	0.154	0.154	0.142	0.156
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.124	0.160	0.160	0.152	0.110	0.110	0.108	0.106
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.102	0.150	0.150	0.154	0.050	0.050	0.116	0.124
54	KT188365.1 <i>Scorpio palmatus</i>	0.176	0.174	0.166	0.160	0.172	0.172	0.172	0.186
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.140	0.172	0.140	0.160	0.142	0.142	0.132	0.144
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.170	0.172	0.146	0.154	0.156	0.156	0.170	0.176
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.164	0.176	0.152	0.170	0.148	0.148	0.166	0.152
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.158	0.180	0.158	0.170	0.160	0.160	0.144	0.152
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.174	0.172	0.164	0.158	0.170	0.170	0.170	0.184
60	EF122607.2 <i>Centruroides vittatus</i>	0.188	0.194	0.164	0.196	0.178	0.178	0.208	0.214
61	EF122608.2 <i>Centruroides vittatus</i>	0.188	0.196	0.166	0.198	0.176	0.176	0.202	0.216
62	EF122612.2 <i>Centruroides vittatus</i>	0.188	0.196	0.162	0.194	0.178	0.178	0.208	0.214
63	EU381064.1 <i>Centruroides vittatus</i>	0.188	0.196	0.162	0.194	0.178	0.178	0.208	0.214
64	EU404114.1 <i>Centruroides vittatus</i>	0.190	0.192	0.162	0.200	0.178	0.178	0.200	0.204
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.184	0.202	0.194	0.194	0.210	0.210	0.210	0.202
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.212	0.200	0.176	0.184	0.212	0.212	0.222	0.210
67	JN018153.1 <i>Lychas mucronatus</i>	0.184	0.212	0.192	0.186	0.196	0.196	0.200	0.198
68	JN018154.1 <i>Parabuthus laevisfrons</i>	0.182	0.196	0.178	0.198	0.182	0.182	0.194	0.204
69	JN018210.1 <i>Lychas mucronatus</i>	0.180	0.218	0.194	0.184	0.180	0.180	0.182	0.192
70	JN018211.1 <i>Lychas mucronatus</i>	0.188	0.226	0.200	0.194	0.198	0.198	0.196	0.204
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.196	0.200	0.180	0.206	0.202	0.202	0.206	0.202
72	KT716037.1 <i>Lychas tricarinatus</i>	0.198	0.220	0.206	0.186	0.200	0.200	0.200	0.200

		25	26	27	28	29	30	31	32
73	KX648425.1 <i>Hottentotta minax</i>	0.198	0.226	0.200	0.228	0.214	0.214	0.202	0.208
74	KX648429.1 <i>Compsobuthus weneri</i>	0.198	0.226	0.200	0.228	0.214	0.214	0.202	0.208
75	KY982184.1 <i>Centruroides schmidt</i>	0.176	0.176	0.188	0.190	0.180	0.180	0.194	0.196
76	KY982185.1 <i>Centruroides vittatus</i>	0.184	0.188	0.160	0.196	0.178	0.178	0.200	0.206
77	KY982187.1 <i>Heteroctenus abudi</i>	0.196	0.198	0.176	0.190	0.184	0.184	0.188	0.182
78	KY982188.1 <i>Heteroctenus abudi</i>	0.198	0.198	0.174	0.190	0.186	0.186	0.188	0.188
79	KY982192.1 <i>Heteroctenus junceus</i>	0.182	0.190	0.176	0.200	0.198	0.198	0.200	0.202
80	KY982193.1 <i>Heteroctenus junceus</i>	0.182	0.190	0.176	0.196	0.198	0.198	0.196	0.198
81	KY982194.1 <i>Heteroctenus junceus</i>	0.182	0.188	0.174	0.188	0.200	0.200	0.194	0.190
82	KY982199.1 <i>Heteroctenus junceus</i>	0.178	0.184	0.176	0.192	0.184	0.184	0.200	0.196
83	KY982273.1 <i>Zabius fuscus</i>	0.186	0.218	0.190	0.202	0.200	0.200	0.210	0.202
84	MF422313.1 <i>Isometrus</i> sp.	0.196	0.212	0.202	0.208	0.210	0.210	0.210	0.214
85	MF422319.1 <i>Lychas tricarinatus</i>	0.194	0.222	0.196	0.188	0.200	0.200	0.196	0.200
86	MF422320.1 <i>Lychas tricarinatus</i>	0.190	0.218	0.196	0.188	0.198	0.198	0.196	0.196
87	MF422321.1 <i>Lychas tricarinatus</i>	0.188	0.216	0.198	0.186	0.194	0.194	0.194	0.194
88	MF422322.1 <i>Lychas tricarinatus</i>	0.190	0.218	0.196	0.188	0.198	0.198	0.196	0.196
89	MF422326.1 <i>Lychas tricarinatus</i>	0.200	0.222	0.198	0.196	0.202	0.202	0.210	0.196
90	MF422327.1 <i>Lychas tricarinatus</i>	0.190	0.214	0.192	0.194	0.200	0.200	0.206	0.202
91	MF422328.1 <i>Lychas tricarinatus</i>	0.192	0.222	0.194	0.186	0.204	0.204	0.210	0.204
92	MF422329.1 <i>Lychas tricarinatus</i>	0.188	0.216	0.192	0.196	0.202	0.202	0.208	0.204
93	MF422330.1 <i>Lychas tricarinatus</i>	0.190	0.214	0.192	0.194	0.200	0.200	0.206	0.202
94	MK479161.1 <i>Centruroides arctimanus</i>	0.192	0.204	0.184	0.202	0.192	0.192	0.204	0.200
95	MK479165.1 <i>Centruroides barbudensis</i>	0.188	0.194	0.168	0.196	0.190	0.190	0.216	0.212
96	MK479171.1 <i>Centruroides exilimanus</i>	0.176	0.206	0.178	0.196	0.190	0.190	0.190	0.194
97	MK479180.1 <i>Centruroides insulanus</i>	0.178	0.170	0.166	0.180	0.190	0.190	0.186	0.196
98	MK479188.1 <i>Centruroides morenoi</i>	0.186	0.188	0.164	0.170	0.186	0.186	0.208	0.202
99	MK479196.1 <i>Centruroides platnicki</i>	0.186	0.182	0.170	0.192	0.170	0.170	0.194	0.204
100	MK479202.1 <i>Centruroides simplex</i>	0.176	0.176	0.168	0.184	0.172	0.172	0.190	0.204
101	MK479204.1 <i>Centruroides taino</i>	0.184	0.192	0.156	0.182	0.184	0.184	0.194	0.208
102	MK479207.1 <i>Centruroides testaceus</i>	0.166	0.186	0.170	0.180	0.168	0.168	0.194	0.196
103	MK479210.1 <i>Centruroides vittatus</i>	0.192	0.194	0.164	0.202	0.180	0.180	0.202	0.206
104	NC 037222.1 <i>Centruroides vittatus</i>	0.192	0.194	0.164	0.202	0.180	0.180	0.202	0.206
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.156	0.190	0.160	0.148	0.156	0.156	0.150	0.148
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.182	0.212	0.198	0.206	0.180	0.180	0.196	0.204
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.156	0.210	0.178	0.186	0.172	0.172	0.156	0.150
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.144	0.168	0.150	0.132	0.154	0.154	0.142	0.156

		33	34	35	36	37	38	39	40
1	PP07	0.017	0.018	0.018	0.018	0.017	0.018	0.018	0.018
2	PP08	0.017	0.018	0.018	0.017	0.017	0.017	0.018	0.017
3	PP11	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.017	0.018	0.018	0.017	0.017	0.018	0.018	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
6	<i>Urodacus varians</i> PC03	0.016	0.015	0.016	0.017	0.016	0.016	0.017	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.017	0.018	0.018	0.017	0.017	0.018	0.018	0.017
8	<i>Urodacus</i> sp Telfer PC05	0.015	0.016	0.015	0.016	0.016	0.016	0.017	0.017
9	<i>Lychas annulatus</i> clade A PC06	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
10	<i>Urodacus yaschenkoki</i> PC07	0.016	0.015	0.015	0.016	0.015	0.016	0.016	0.016
11	<i>Urodacus yaschenkoki</i> PC08	0.016	0.015	0.015	0.016	0.015	0.016	0.016	0.016
12	<i>Lychas annulatus</i> clade B NN01	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
14	<i>Lychas annulatus</i> clade B NN04	0.017	0.018	0.018	0.018	0.017	0.018	0.018	0.018
15	<i>Lychas annulatus</i> NN05 clade A	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
16	<i>Lychas annulatus</i> clade A NN06	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
17	<i>Lychas annulatus</i> clade A NN07	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
18	<i>Lychas annulatus</i> clade A NN08	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
19	<i>Lychas annulatus</i> clade B NN09	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
20	<i>Lychas annulatus</i> clade ANN10	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
21	EF122605.2 <i>Centruroides vittatus</i>	0.018	0.017	0.018	0.017	0.017	0.018	0.018	0.018
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.015	0.016	0.015	0.016	0.016	0.016	0.017	0.016
23	KT446990. <i>Brachistosternus paposo</i>	0.016	0.016	0.015	0.008	0.013	0.013	0.016	0.014
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.016	0.016	0.016	0.011	0.014	0.014	0.016	0.014
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.016	0.016	0.016	0.014	0.013	0.014	0.017	0.011
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.015	0.016	0.014	0.016	0.016	0.017	0.017	0.016
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.015	0.015	0.014	0.016	0.015	0.015	0.017	0.015
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.012	0.016	0.014	0.016	0.015	0.015	0.017	0.016
29	KX517230.1 <i>Brachistosternus paposo</i>	0.016	0.016	0.015	0.008	0.013	0.013	0.016	0.014
30	KX517229.1 <i>Brachistosternus paposo</i>	0.016	0.016	0.015	0.008	0.013	0.013	0.016	0.014
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.016	0.016	0.015	0.014	0.013	0.011	0.016	0.014
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.016	0.016	0.016	0.014	0.014	0.012	0.017	0.014
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030		0.016	0.015	0.016	0.015	0.016	0.017	0.016
34	AY156581.1 <i>Pandinus dictator</i>	0.158		0.015	0.017	0.017	0.016	0.017	0.016
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.120	0.132		0.016	0.016	0.016	0.017	0.016
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.144	0.174	0.140		0.013	0.014	0.016	0.014

		33	34	35	36	37	38	39	40
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.132	0.164	0.146	0.100		0.014	0.016	0.013
38	KT446946.1 <i>Brachistosternus chango</i>	0.146	0.160	0.154	0.106	0.118		0.016	0.015
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.174	0.178	0.176	0.160	0.142	0.150		0.017
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.148	0.150	0.146	0.116	0.094	0.122	0.178	
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.140	0.098	0.158	0.158	0.178	0.166	0.182	0.180
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.124	0.152	0.106	0.142	0.148	0.162	0.180	0.154
43	KX517244.1 <i>Brachistosternus paposo</i>	0.146	0.164	0.140	0.028	0.100	0.102	0.152	0.116
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.148	0.164	0.142	0.104	0.120	0.104	0.166	0.112
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.152	0.164	0.144	0.056	0.102	0.104	0.164	0.110
46	KT446986.1 <i>Brachistosternus negrei</i>	0.156	0.164	0.138	0.120	0.102	0.080	0.154	0.118
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.130	0.158	0.142	0.106	0.018	0.112	0.146	0.094
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.158	0.174	0.166	0.168	0.132	0.150	0.118	0.166
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.158	0.154	0.148	0.114	0.124	0.130	0.142	0.122
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.122	0.148	0.136	0.168	0.142	0.164	0.174	0.148
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.142	0.154	0.140	0.160	0.140	0.158	0.164	0.150
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.152	0.172	0.160	0.116	0.124	0.096	0.148	0.138
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.154	0.172	0.152	0.050	0.106	0.114	0.162	0.110
54	KT188365.1 <i>Scorpio palmatus</i>	0.160	0.160	0.174	0.188	0.164	0.168	0.166	0.172
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.164	0.154	0.178	0.162	0.134	0.132	0.144	0.158
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.168	0.126	0.164	0.166	0.166	0.168	0.176	0.180
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.162	0.168	0.174	0.162	0.168	0.160	0.102	0.172
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.158	0.180	0.162	0.160	0.148	0.160	0.138	0.150
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.162	0.160	0.172	0.186	0.162	0.166	0.164	0.170
60	EF122607.2 <i>Centruroides vittatus</i>	0.200	0.180	0.198	0.186	0.184	0.192	0.198	0.194
61	EF122608.2 <i>Centruroides vittatus</i>	0.204	0.186	0.202	0.186	0.182	0.192	0.192	0.198
62	EF122612.2 <i>Centruroides vittatus</i>	0.198	0.178	0.194	0.186	0.184	0.192	0.200	0.194
63	EU381064.1 <i>Centruroides vittatus</i>	0.198	0.178	0.196	0.186	0.184	0.192	0.200	0.194
64	EU404114.1 <i>Centruroides vittatus</i>	0.204	0.184	0.202	0.182	0.182	0.204	0.200	0.192
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.200	0.208	0.210	0.208	0.202	0.202	0.226	0.200
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.208	0.188	0.202	0.212	0.220	0.200	0.210	0.204
67	JN018153.1 <i>Lychas mucronatus</i>	0.196	0.198	0.202	0.206	0.202	0.186	0.206	0.204
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.212	0.206	0.200	0.192	0.194	0.204	0.204	0.188
69	JN018210.1 <i>Lychas mucronatus</i>	0.184	0.198	0.204	0.196	0.164	0.182	0.216	0.180
70	JN018211.1 <i>Lychas mucronatus</i>	0.200	0.216	0.208	0.212	0.204	0.196	0.218	0.208
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.196	0.176	0.198	0.212	0.202	0.202	0.216	0.202
72	KT716037.1 <i>Lychas tricarinatus</i>	0.190	0.210	0.200	0.206	0.194	0.206	0.218	0.212

		33	34	35	36	37	38	39	40
73	KX648425.1 <i>Hottentotta minax</i>	0.226	0.204	0.212	0.210	0.218	0.212	0.244	0.196
74	KX648429.1 <i>Compsobuthus weneri</i>	0.226	0.204	0.212	0.210	0.218	0.212	0.244	0.196
75	KY982184.1 <i>Centruroides schmidt</i>	0.186	0.172	0.176	0.174	0.180	0.200	0.198	0.198
76	KY982185.1 <i>Centruroides vittatus</i>	0.200	0.180	0.198	0.182	0.182	0.198	0.200	0.190
77	KY982187.1 <i>Heteroctenus abudi</i>	0.184	0.172	0.174	0.192	0.194	0.182	0.206	0.190
78	KY982188.1 <i>Heteroctenus abudi</i>	0.188	0.170	0.172	0.198	0.196	0.190	0.212	0.188
79	KY982192.1 <i>Heteroctenus junceus</i>	0.184	0.184	0.184	0.190	0.200	0.202	0.216	0.178
80	KY982193.1 <i>Heteroctenus junceus</i>	0.180	0.180	0.180	0.190	0.200	0.202	0.218	0.174
81	KY982194.1 <i>Heteroctenus junceus</i>	0.182	0.168	0.174	0.194	0.194	0.202	0.214	0.176
82	KY982199.1 <i>Heteroctenus junceus</i>	0.174	0.174	0.180	0.190	0.196	0.206	0.226	0.170
83	KY982273.1 <i>Zabius fuscus</i>	0.224	0.202	0.210	0.200	0.204	0.198	0.216	0.186
84	MF422313.1 <i>Isometrus</i> sp.	0.198	0.214	0.224	0.208	0.192	0.200	0.226	0.210
85	MF422319.1 <i>Lychas tricarinatus</i>	0.190	0.208	0.200	0.210	0.198	0.202	0.222	0.216
86	MF422320.1 <i>Lychas tricarinatus</i>	0.192	0.208	0.202	0.208	0.198	0.202	0.224	0.212
87	MF422321.1 <i>Lychas tricarinatus</i>	0.190	0.206	0.198	0.204	0.196	0.200	0.220	0.210
88	MF422322.1 <i>Lychas tricarinatus</i>	0.192	0.208	0.202	0.208	0.198	0.202	0.224	0.212
89	MF422326.1 <i>Lychas tricarinatus</i>	0.212	0.196	0.210	0.212	0.210	0.198	0.220	0.214
90	MF422327.1 <i>Lychas tricarinatus</i>	0.196	0.202	0.204	0.206	0.210	0.198	0.226	0.214
91	MF422328.1 <i>Lychas tricarinatus</i>	0.202	0.204	0.208	0.216	0.212	0.200	0.220	0.210
92	MF422329.1 <i>Lychas tricarinatus</i>	0.198	0.202	0.206	0.208	0.208	0.200	0.224	0.216
93	MF422330.1 <i>Lychas tricarinatus</i>	0.196	0.202	0.204	0.206	0.210	0.198	0.226	0.214
94	MK479161.1 <i>Centruroides arctimanus</i>	0.192	0.186	0.194	0.184	0.200	0.204	0.216	0.194
95	MK479165.1 <i>Centruroides barbudensis</i>	0.204	0.196	0.200	0.196	0.204	0.206	0.226	0.188
96	MK479171.1 <i>Centruroides exilimanus</i>	0.206	0.172	0.204	0.192	0.192	0.196	0.218	0.180
97	MK479180.1 <i>Centruroides insulanus</i>	0.176	0.160	0.180	0.190	0.196	0.188	0.194	0.174
98	MK479188.1 <i>Centruroides morenoi</i>	0.174	0.170	0.192	0.188	0.198	0.186	0.212	0.190
99	MK479196.1 <i>Centruroides platnicki</i>	0.196	0.182	0.178	0.174	0.186	0.186	0.214	0.178
100	MK479202.1 <i>Centruroides simplex</i>	0.184	0.160	0.172	0.170	0.174	0.190	0.190	0.174
101	MK479204.1 <i>Centruroides taino</i>	0.192	0.174	0.184	0.196	0.188	0.188	0.198	0.190
102	MK479207.1 <i>Centruroides testaceus</i>	0.190	0.162	0.186	0.180	0.178	0.202	0.202	0.178
103	MK479210.1 <i>Centruroides vittatus</i>	0.206	0.186	0.204	0.184	0.184	0.206	0.202	0.194
104	NC 037222.1 <i>Centruroides vittatus</i>	0.206	0.186	0.204	0.184	0.184	0.206	0.202	0.194
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.144	0.182	0.164	0.162	0.146	0.148	0.158	0.166
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.198	0.202	0.216	0.180	0.184	0.206	0.214	0.188
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.176	0.172	0.188	0.174	0.150	0.156	0.174	0.160
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.142	0.154	0.140	0.160	0.140	0.158	0.164	0.150

		41	42	43	44	45	46	47	48
1	PP07	0.018	0.018	0.017	0.018	0.017	0.018	0.016	0.017
2	PP08	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
3	PP11	0.018	0.018	0.018	0.018	0.017	0.018	0.016	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.018	0.018	0.017	0.018	0.017	0.018	0.017	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.016	0.017	0.016	0.017	0.017	0.016	0.016	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.018	0.018	0.017	0.018	0.017	0.018	0.017	0.017
8	<i>Urodacus</i> sp Telfer PC05	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
9	<i>Lychas annulatus</i> clade A PC06	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
11	<i>Urodacus yaschenkoki</i> PC08	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
12	<i>Lychas annulatus</i> clade B NN01	0.019	0.018	0.018	0.018	0.017	0.018	0.017	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.018	0.018	0.017	0.018	0.017	0.018	0.017	0.017
15	<i>Lychas annulatus</i> NN05 clade A	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.018	0.018	0.018	0.018	0.017	0.018	0.017	0.017
20	<i>Lychas annulatus</i> clade ANN10	0.018	0.018	0.017	0.018	0.018	0.017	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.017	0.017	0.017	0.018	0.017	0.018	0.018	0.018
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
23	KT446990. <i>Brachistosternus paposo</i>	0.016	0.015	0.007	0.014	0.010	0.014	0.013	0.016
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.016	0.016	0.010	0.014	0.010	0.014	0.015	0.016
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.016	0.014	0.015	0.014	0.015	0.013	0.016
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.016	0.015	0.016	0.017	0.016	0.017	0.016	0.017
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.015	0.015	0.016	0.016	0.016	0.016	0.015	0.016
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.016	0.016	0.016	0.017	0.016	0.016	0.015	0.016
29	KX517230.1 <i>Brachistosternus paposo</i>	0.016	0.015	0.007	0.014	0.010	0.014	0.013	0.016
30	KX517229.1 <i>Brachistosternus paposo</i>	0.016	0.015	0.007	0.014	0.010	0.014	0.013	0.016
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.017	0.016	0.014	0.013	0.014	0.011	0.013	0.016
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.017	0.017	0.015	0.013	0.015	0.012	0.014	0.016
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.016	0.015	0.016	0.016	0.016	0.016	0.015	0.016
34	AY156581.1 <i>Pandinus dictator</i>	0.013	0.016	0.017	0.017	0.017	0.017	0.016	0.017
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.016	0.014	0.016	0.016	0.016	0.015	0.016	0.017
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.016	0.016	0.007	0.014	0.010	0.015	0.014	0.017

		41	42	43	44	45	46	47	48
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.016	0.013	0.015	0.014	0.014	0.006	0.015
38	KT446946.1 <i>Brachistosternus chango</i>	0.017	0.016	0.014	0.014	0.014	0.012	0.014	0.016
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.017	0.017	0.016	0.017	0.017	0.016	0.016	0.014
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.017	0.016	0.014	0.014	0.014	0.014	0.013	0.017
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050		0.016	0.016	0.017	0.016	0.017	0.017	0.017
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.154		0.015	0.016	0.016	0.016	0.016	0.017
43	KX517244.1 <i>Brachistosternus paposo</i>	0.144	0.136		0.013	0.010	0.014	0.014	0.016
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.182	0.154	0.100		0.014	0.013	0.014	0.016
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.162	0.148	0.052	0.108		0.014	0.014	0.016
46	KT446986.1 <i>Brachistosternus negrei</i>	0.168	0.162	0.118	0.100	0.108		0.013	0.016
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.178	0.146	0.106	0.116	0.106	0.100		0.015
48	JX909544.1 <i>Paruroctonus boreus</i> SKY42/AMNH	0.168	0.178	0.154	0.162	0.156	0.152	0.136	
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.162	0.156	0.112	0.120	0.118	0.108	0.120	0.156
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.150	0.158	0.164	0.146	0.160	0.154	0.140	0.160
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.160	0.152	0.160	0.170	0.168	0.128	0.138	0.166
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.180	0.176	0.118	0.108	0.116	0.098	0.128	0.162
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.160	0.148	0.042	0.102	0.026	0.118	0.112	0.154
54	KT188365.1 <i>Scorpio palmatus</i>	0.164	0.186	0.178	0.190	0.180	0.178	0.162	0.172
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.158	0.172	0.162	0.152	0.156	0.152	0.138	0.148
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.132	0.158	0.158	0.194	0.164	0.164	0.162	0.172
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.150	0.172	0.152	0.158	0.178	0.156	0.172	0.120
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.176	0.160	0.156	0.148	0.178	0.162	0.146	0.092
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.164	0.184	0.176	0.188	0.178	0.176	0.160	0.170
60	EF122607.2 <i>Centruroides vittatus</i>	0.186	0.186	0.178	0.198	0.178	0.198	0.190	0.196
61	EF122608.2 <i>Centruroides vittatus</i>	0.184	0.186	0.178	0.202	0.186	0.196	0.190	0.196
62	EF122612.2 <i>Centruroides vittatus</i>	0.184	0.190	0.178	0.198	0.178	0.198	0.190	0.198
63	EU381064.1 <i>Centruroides vittatus</i>	0.184	0.188	0.178	0.198	0.178	0.198	0.190	0.198
64	EU404114.1 <i>Centruroides vittatus</i>	0.182	0.192	0.178	0.198	0.180	0.192	0.190	0.210
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.222	0.222	0.212	0.214	0.208	0.202	0.200	0.214
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.212	0.214	0.212	0.232	0.216	0.218	0.216	0.206
67	JN018153.1 <i>Lychas mucronatus</i>	0.198	0.202	0.202	0.212	0.194	0.196	0.200	0.188
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.208	0.210	0.190	0.192	0.182	0.200	0.190	0.190
69	JN018210.1 <i>Lychas mucronatus</i>	0.204	0.208	0.184	0.204	0.196	0.172	0.166	0.196
70	JN018211.1 <i>Lychas mucronatus</i>	0.210	0.212	0.204	0.210	0.198	0.194	0.200	0.212
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.206	0.200	0.204	0.210	0.194	0.202	0.206	0.214
72	KT716037.1 <i>Lychas tricarinatus</i>	0.208	0.224	0.208	0.206	0.206	0.194	0.192	0.204

		41	42	43	44	45	46	47	48
73	KX648425.1 <i>Hottentotta minax</i>	0.210	0.232	0.208	0.216	0.208	0.220	0.214	0.216
74	KX648429.1 <i>Compsobuthus weneri</i>	0.210	0.232	0.208	0.216	0.208	0.220	0.214	0.216
75	KY982184.1 <i>Centruroides schmidt</i>	0.164	0.188	0.176	0.190	0.188	0.194	0.172	0.186
76	KY982185.1 <i>Centruroides vittatus</i>	0.178	0.186	0.178	0.196	0.176	0.196	0.188	0.204
77	KY982187.1 <i>Heteroctenus abudi</i>	0.190	0.196	0.188	0.196	0.188	0.180	0.188	0.196
78	KY982188.1 <i>Heteroctenus abudi</i>	0.192	0.194	0.194	0.194	0.190	0.180	0.190	0.196
79	KY982192.1 <i>Heteroctenus junceus</i>	0.188	0.190	0.192	0.196	0.192	0.206	0.202	0.206
80	KY982193.1 <i>Heteroctenus junceus</i>	0.188	0.186	0.192	0.196	0.192	0.202	0.198	0.208
81	KY982194.1 <i>Heteroctenus junceus</i>	0.188	0.198	0.194	0.204	0.190	0.194	0.186	0.200
82	KY982199.1 <i>Heteroctenus junceus</i>	0.182	0.178	0.188	0.184	0.184	0.208	0.194	0.202
83	KY982273.1 <i>Zabius fuscus</i>	0.202	0.204	0.194	0.218	0.200	0.210	0.198	0.198
84	MF422313.1 <i>Isometrus</i> sp.	0.204	0.222	0.208	0.228	0.206	0.220	0.196	0.212
85	MF422319.1 <i>Lychas tricarinatus</i>	0.210	0.226	0.208	0.208	0.202	0.190	0.196	0.198
86	MF422320.1 <i>Lychas tricarinatus</i>	0.206	0.224	0.206	0.208	0.204	0.192	0.196	0.196
87	MF422321.1 <i>Lychas tricarinatus</i>	0.204	0.220	0.202	0.208	0.200	0.188	0.194	0.194
88	MF422322.1 <i>Lychas tricarinatus</i>	0.206	0.224	0.206	0.208	0.204	0.192	0.196	0.196
89	MF422326.1 <i>Lychas tricarinatus</i>	0.216	0.226	0.210	0.212	0.206	0.200	0.206	0.200
90	MF422327.1 <i>Lychas tricarinatus</i>	0.204	0.220	0.204	0.210	0.202	0.200	0.202	0.202
91	MF422328.1 <i>Lychas tricarinatus</i>	0.216	0.226	0.210	0.214	0.206	0.200	0.208	0.198
92	MF422329.1 <i>Lychas tricarinatus</i>	0.204	0.222	0.206	0.212	0.204	0.202	0.200	0.202
93	MF422330.1 <i>Lychas tricarinatus</i>	0.204	0.220	0.204	0.210	0.202	0.200	0.202	0.202
94	MK479161.1 <i>Centruroides arctimanus</i>	0.184	0.202	0.194	0.214	0.192	0.210	0.202	0.198
95	MK479165.1 <i>Centruroides barbudensis</i>	0.182	0.194	0.194	0.208	0.190	0.212	0.204	0.198
96	MK479171.1 <i>Centruroides exilimanus</i>	0.180	0.210	0.186	0.210	0.190	0.212	0.196	0.196
97	MK479180.1 <i>Centruroides insulanus</i>	0.176	0.188	0.192	0.192	0.186	0.186	0.188	0.200
98	MK479188.1 <i>Centruroides morenoi</i>	0.156	0.190	0.182	0.202	0.180	0.198	0.198	0.198
99	MK479196.1 <i>Centruroides platnicki</i>	0.184	0.194	0.174	0.194	0.178	0.188	0.182	0.190
100	MK479202.1 <i>Centruroides simplex</i>	0.170	0.176	0.168	0.184	0.176	0.204	0.176	0.202
101	MK479204.1 <i>Centruroides taino</i>	0.190	0.196	0.190	0.206	0.184	0.194	0.188	0.182
102	MK479207.1 <i>Centruroides testaceus</i>	0.168	0.188	0.172	0.190	0.170	0.212	0.178	0.186
103	MK479210.1 <i>Centruroides vittatus</i>	0.184	0.194	0.180	0.200	0.182	0.194	0.192	0.212
104	NC 037222.1 <i>Centruroides vittatus</i>	0.184	0.194	0.180	0.200	0.182	0.194	0.192	0.212
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.186	0.172	0.160	0.156	0.174	0.144	0.148	0.162
106	JN018163.1 <i>Chaerilus juliettea</i> voucher MNHN-JAB32	0.208	0.214	0.176	0.188	0.180	0.206	0.190	0.194
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.198	0.182	0.172	0.166	0.176	0.140	0.144	0.190
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.160	0.152	0.160	0.170	0.168	0.128	0.138	0.166

		49	50	51	52	53	54	55	56
1	PP07	0.018	0.017	0.018	0.018	0.017	0.018	0.018	0.018
2	PP08	0.018	0.017	0.017	0.018	0.017	0.017	0.017	0.017
3	PP11	0.018	0.017	0.018	0.018	0.017	0.018	0.018	0.018
4	<i>Lychas annulatus</i> clade B PC01	0.018	0.018	0.017	0.018	0.017	0.018	0.017	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
6	<i>Urodacus varians</i> PC03	0.016	0.016	0.016	0.017	0.017	0.016	0.016	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.018	0.018	0.017	0.019	0.017	0.018	0.018	0.018
8	<i>Urodacus</i> sp Telfer PC05	0.016	0.015	0.016	0.017	0.017	0.017	0.016	0.016
9	<i>Lychas annulatus</i> clade A PC06	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
11	<i>Urodacus yaschenkoki</i> PC08	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
12	<i>Lychas annulatus</i> clade B NN01	0.018	0.018	0.018	0.019	0.017	0.018	0.018	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.018	0.017	0.018	0.018	0.017	0.018	0.018	0.018
15	<i>Lychas annulatus</i> NN05 clade A	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.018	0.017	0.018	0.018	0.017	0.018	0.018	0.018
20	<i>Lychas annulatus</i> clade ANN10	0.018	0.017	0.017	0.018	0.017	0.018	0.018	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.018	0.018	0.017	0.019	0.018	0.017	0.017	0.017
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.015	0.016	0.015	0.016	0.016	0.017	0.016	0.016
23	KT446990. <i>Brachistosternus paposo</i>	0.014	0.017	0.016	0.014	0.010	0.017	0.016	0.016
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.015	0.017	0.017	0.014	0.010	0.017	0.016	0.016
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.015	0.016	0.016	0.015	0.014	0.017	0.016	0.017
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.016	0.016	0.017	0.016	0.016	0.017	0.017	0.017
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.016	0.014	0.016	0.016	0.016	0.017	0.016	0.016
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.016	0.015	0.015	0.016	0.016	0.016	0.016	0.016
29	KX517230.1 <i>Brachistosternus paposo</i>	0.014	0.017	0.016	0.014	0.010	0.017	0.016	0.016
30	KX517229.1 <i>Brachistosternus paposo</i>	0.014	0.017	0.016	0.014	0.010	0.017	0.016	0.016
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.015	0.016	0.016	0.014	0.014	0.017	0.015	0.017
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.015	0.016	0.016	0.014	0.015	0.017	0.016	0.017
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.016	0.015	0.016	0.016	0.016	0.016	0.017	0.017
34	AY156581.1 <i>Pandinus dictator</i>	0.016	0.016	0.016	0.017	0.017	0.016	0.016	0.015
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.016	0.015	0.016	0.016	0.016	0.017	0.017	0.017
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.014	0.017	0.016	0.014	0.010	0.017	0.016	0.017

		49	50	51	52	53	54	55	56
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.015	0.016	0.016	0.015	0.014	0.017	0.015	0.017
38	KT446946.1 <i>Brachistosternus chango</i>	0.015	0.017	0.016	0.013	0.014	0.017	0.015	0.017
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.016	0.017	0.017	0.016	0.016	0.017	0.016	0.017
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.015	0.016	0.016	0.015	0.014	0.017	0.016	0.017
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.016	0.016	0.016	0.017	0.016	0.017	0.016	0.015
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.016	0.016	0.016	0.017	0.016	0.017	0.017	0.016
43	KX517244.1 <i>Brachistosternus paposo</i>	0.014	0.017	0.016	0.014	0.009	0.017	0.016	0.016
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.015	0.016	0.017	0.014	0.014	0.018	0.016	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.014	0.016	0.017	0.014	0.007	0.017	0.016	0.017
46	KT446986.1 <i>Brachistosternus negrei</i>	0.014	0.016	0.015	0.013	0.014	0.017	0.016	0.017
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.015	0.016	0.015	0.015	0.014	0.016	0.015	0.016
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.016	0.016	0.017	0.016	0.016	0.017	0.016	0.017
49	KT446960.1 <i>Brachistosternus ferrugineus</i>		0.016	0.016	0.015	0.015	0.018	0.016	0.017
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.154		0.016	0.017	0.016	0.016	0.016	0.017
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.146	0.154		0.016	0.017	0.016	0.016	0.016
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.136	0.168	0.160		0.014	0.018	0.017	0.017
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.122	0.158	0.170	0.116		0.017	0.017	0.017
54	KT188365.1 <i>Scorpio palmatus</i>	0.190	0.162	0.148	0.190	0.184		0.017	0.016
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.148	0.154	0.158	0.164	0.164	0.170		0.016
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.168	0.172	0.152	0.186	0.178	0.146	0.152	
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.132	0.156	0.174	0.172	0.176	0.172	0.134	0.174
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.160	0.164	0.174	0.168	0.172	0.180	0.152	0.176
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.190	0.162	0.146	0.188	0.182	0.002	0.168	0.144
60	EF122607.2 <i>Centruroides vittatus</i>	0.192	0.194	0.186	0.222	0.190	0.188	0.188	0.172
61	EF122608.2 <i>Centruroides vittatus</i>	0.194	0.200	0.186	0.216	0.190	0.188	0.184	0.180
62	EF122612.2 <i>Centruroides vittatus</i>	0.192	0.192	0.188	0.222	0.190	0.188	0.188	0.176
63	EU381064.1 <i>Centruroides vittatus</i>	0.192	0.192	0.188	0.222	0.190	0.186	0.188	0.174
64	EU404114.1 <i>Centruroides vittatus</i>	0.188	0.192	0.192	0.216	0.190	0.190	0.188	0.178
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.198	0.190	0.206	0.226	0.208	0.194	0.212	0.204
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.198	0.202	0.216	0.226	0.228	0.214	0.200	0.180
67	JN018153.1 <i>Lychas mucronatus</i>	0.210	0.192	0.204	0.226	0.196	0.200	0.186	0.196
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.192	0.192	0.208	0.214	0.192	0.222	0.192	0.200
69	JN018210.1 <i>Lychas mucronatus</i>	0.210	0.198	0.174	0.198	0.190	0.192	0.198	0.188
70	JN018211.1 <i>Lychas mucronatus</i>	0.208	0.220	0.206	0.206	0.208	0.220	0.200	0.188
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.202	0.190	0.212	0.228	0.202	0.220	0.202	0.196
72	KT716037.1 <i>Lychas tricarinatus</i>	0.200	0.192	0.188	0.198	0.204	0.198	0.224	0.196

		49	50	51	52	53	54	55	56
73	KX648425.1 <i>Hottentotta minax</i>	0.212	0.200	0.226	0.238	0.214	0.234	0.218	0.214
74	KX648429.1 <i>Compsobuthus weneri</i>	0.212	0.200	0.226	0.238	0.214	0.234	0.218	0.214
75	KY982184.1 <i>Centruroides schmidt</i>	0.190	0.178	0.202	0.202	0.182	0.208	0.192	0.198
76	KY982185.1 <i>Centruroides vittatus</i>	0.186	0.188	0.190	0.214	0.186	0.192	0.184	0.170
77	KY982187.1 <i>Heteroctenus abudi</i>	0.176	0.180	0.204	0.202	0.192	0.198	0.194	0.184
78	KY982188.1 <i>Heteroctenus abudi</i>	0.174	0.178	0.204	0.202	0.194	0.200	0.198	0.186
79	KY982192.1 <i>Heteroctenus junceus</i>	0.172	0.184	0.198	0.212	0.198	0.210	0.184	0.194
80	KY982193.1 <i>Heteroctenus junceus</i>	0.176	0.180	0.194	0.212	0.198	0.208	0.188	0.190
81	KY982194.1 <i>Heteroctenus junceus</i>	0.174	0.182	0.196	0.214	0.190	0.200	0.188	0.186
82	KY982199.1 <i>Heteroctenus junceus</i>	0.174	0.172	0.188	0.210	0.190	0.194	0.186	0.188
83	KY982273.1 <i>Zabius fuscus</i>	0.188	0.202	0.200	0.222	0.196	0.210	0.216	0.226
84	MF422313.1 <i>Isometrus</i> sp.	0.216	0.204	0.210	0.228	0.212	0.212	0.208	0.192
85	MF422319.1 <i>Lychas tricarinatus</i>	0.198	0.194	0.198	0.204	0.204	0.204	0.222	0.196
86	MF422320.1 <i>Lychas tricarinatus</i>	0.198	0.192	0.198	0.202	0.202	0.204	0.224	0.196
87	MF422321.1 <i>Lychas tricarinatus</i>	0.194	0.192	0.194	0.200	0.198	0.200	0.220	0.192
88	MF422322.1 <i>Lychas tricarinatus</i>	0.198	0.192	0.198	0.202	0.202	0.204	0.224	0.196
89	MF422326.1 <i>Lychas tricarinatus</i>	0.204	0.190	0.206	0.228	0.204	0.204	0.218	0.202
90	MF422327.1 <i>Lychas tricarinatus</i>	0.206	0.188	0.208	0.218	0.204	0.198	0.224	0.208
91	MF422328.1 <i>Lychas tricarinatus</i>	0.204	0.188	0.206	0.228	0.210	0.200	0.214	0.208
92	MF422329.1 <i>Lychas tricarinatus</i>	0.206	0.188	0.210	0.220	0.206	0.200	0.224	0.210
93	MF422330.1 <i>Lychas tricarinatus</i>	0.206	0.188	0.208	0.218	0.204	0.198	0.224	0.208
94	MK479161.1 <i>Centruroides arctimanus</i>	0.178	0.196	0.206	0.210	0.194	0.208	0.196	0.200
95	MK479165.1 <i>Centruroides barbudensis</i>	0.202	0.196	0.216	0.214	0.190	0.196	0.190	0.192
96	MK479171.1 <i>Centruroides exilimanus</i>	0.190	0.190	0.188	0.226	0.192	0.206	0.190	0.208
97	MK479180.1 <i>Centruroides insulanus</i>	0.180	0.170	0.190	0.200	0.190	0.190	0.194	0.178
98	MK479188.1 <i>Centruroides morenoi</i>	0.202	0.186	0.200	0.212	0.186	0.206	0.202	0.176
99	MK479196.1 <i>Centruroides platnicki</i>	0.182	0.184	0.190	0.210	0.182	0.202	0.182	0.196
100	MK479202.1 <i>Centruroides simplex</i>	0.184	0.186	0.192	0.220	0.180	0.202	0.192	0.184
101	MK479204.1 <i>Centruroides taino</i>	0.188	0.182	0.204	0.204	0.186	0.206	0.176	0.184
102	MK479207.1 <i>Centruroides testaceus</i>	0.194	0.176	0.190	0.216	0.172	0.208	0.182	0.186
103	MK479210.1 <i>Centruroides vittatus</i>	0.186	0.194	0.194	0.218	0.192	0.192	0.190	0.180
104	NC 037222.1 <i>Centruroides vittatus</i>	0.186	0.194	0.194	0.218	0.192	0.192	0.190	0.180
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.162	0.158	0.162	0.162	0.166	0.188	0.166	0.182
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.192	0.178	0.188	0.216	0.184	0.204	0.206	0.220
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.166	0.176	0.180	0.162	0.176	0.190	0.190	0.196
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.146	0.154	0.000	0.160	0.170	0.148	0.158	0.152

		57	58	59	60	61	62	63	64
1	PP07	0.019	0.018	0.018	0.016	0.016	0.016	0.016	0.017
2	PP08	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
3	PP11	0.019	0.018	0.018	0.017	0.017	0.017	0.017	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.019	0.018	0.018	0.016	0.016	0.016	0.016	0.016
5	<i>Lychas annulatus</i> clade A PC02	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.017	0.017	0.016	0.018	0.018	0.018	0.018	0.018
7	<i>Lychas annulatus</i> clade B PC04	0.019	0.018	0.018	0.016	0.016	0.016	0.016	0.016
8	<i>Urodacus</i> sp Telfer PC05	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.018
9	<i>Lychas annulatus</i> clade A PC06	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.017	0.016	0.016	0.018	0.018	0.018	0.018	0.018
11	<i>Urodacus yaschenkoki</i> PC08	0.017	0.016	0.016	0.018	0.018	0.018	0.018	0.018
12	<i>Lychas annulatus</i> clade B NN01	0.019	0.018	0.018	0.017	0.017	0.017	0.017	0.017
13	<i>Lychas annulatus</i> clade A NN03	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.019	0.018	0.018	0.017	0.017	0.017	0.017	0.017
15	<i>Lychas annulatus</i> NN05 clade A	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.019	0.018	0.018	0.017	0.017	0.017	0.017	0.017
20	<i>Lychas annulatus</i> clade ANN10	0.018	0.018	0.018	0.017	0.018	0.017	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.018	0.018	0.017	0.000	0.006	0.003	0.002	0.008
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.017	0.017	0.016	0.018	0.019	0.018	0.018	0.018
23	KT446990. <i>Brachistosternus paposo</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.017
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.016	0.017	0.017	0.017	0.017	0.017	0.018
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.018
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.016	0.016	0.017	0.017	0.017	0.016	0.016	0.016
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.017	0.017	0.016	0.018	0.018	0.018	0.018	0.018
29	KX517230.1 <i>Brachistosternus paposo</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
30	KX517229.1 <i>Brachistosternus paposo</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.017	0.016	0.017	0.018	0.018	0.018	0.018	0.018
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.016	0.016	0.017	0.018	0.018	0.018	0.018	0.018
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.016	0.016	0.016	0.018	0.018	0.018	0.018	0.018
34	AY156581.1 <i>Pandinus dictator</i>	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.017
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.017	0.016	0.017	0.018	0.018	0.018	0.018	0.018
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017

		57	58	59	60	61	62	63	64
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.016	0.016	0.017	0.017	0.017	0.017	0.017
38	KT446946.1 <i>Brachistosternus chango</i>	0.016	0.016	0.017	0.018	0.018	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.014	0.015	0.017	0.018	0.018	0.018	0.018	0.018
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.017	0.016	0.017	0.018	0.018	0.018	0.018	0.018
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.016	0.017	0.017	0.017	0.017	0.017	0.017	0.017
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.017	0.016	0.017	0.017	0.017	0.018	0.017	0.018
43	KX517244.1 <i>Brachistosternus paposo</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.016	0.016	0.017	0.018	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
46	KT446986.1 <i>Brachistosternus negrei</i>	0.016	0.016	0.017	0.018	0.018	0.018	0.018	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.016	0.016	0.018	0.018	0.018	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.015	0.013	0.017	0.018	0.018	0.018	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.015	0.016	0.018	0.018	0.018	0.018	0.018	0.017
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.016	0.017	0.016	0.018	0.018	0.018	0.018	0.018
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.018
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.017	0.017	0.017	0.019	0.018	0.019	0.019	0.018
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.017	0.017	0.002	0.017	0.017	0.017	0.017	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.015	0.016	0.017	0.017	0.017	0.017	0.017	0.017
56	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.017
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317		0.016	0.017	0.018	0.018	0.018	0.018	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.142		0.017	0.018	0.018	0.018	0.018	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.172	0.180		0.017	0.017	0.017	0.017	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.194	0.194	0.188		0.006	0.003	0.002	0.008
61	EF122608.2 <i>Centruroides vittatus</i>	0.196	0.192	0.188	0.016		0.006	0.006	0.008
62	EF122612.2 <i>Centruroides vittatus</i>	0.194	0.196	0.188	0.004	0.020		0.002	0.008
63	EU381064.1 <i>Centruroides vittatus</i>	0.194	0.196	0.186	0.002	0.018	0.002		0.008
64	EU404114.1 <i>Centruroides vittatus</i>	0.198	0.194	0.190	0.030	0.030	0.034	0.032	
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.238	0.204	0.196	0.170	0.172	0.166	0.168	0.172
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.218	0.220	0.212	0.160	0.164	0.156	0.158	0.166
67	JN018153.1 <i>Lychas mucronatus</i>	0.216	0.204	0.200	0.172	0.176	0.172	0.174	0.180
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.222	0.204	0.222	0.172	0.174	0.170	0.170	0.174
69	JN018210.1 <i>Lychas mucronatus</i>	0.234	0.208	0.190	0.164	0.160	0.164	0.164	0.168
70	JN018211.1 <i>Lychas mucronatus</i>	0.218	0.214	0.220	0.194	0.198	0.196	0.196	0.202
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.222	0.212	0.220	0.158	0.168	0.154	0.156	0.160
72	KT716037.1 <i>Lychas tricarinatus</i>	0.210	0.210	0.198	0.168	0.172	0.166	0.166	0.168

		57	58	59	60	61	62	63	64
73	KX648425.1 <i>Hottentotta minax</i>	0.230	0.208	0.236	0.188	0.192	0.186	0.186	0.190
74	KX648429.1 <i>Compsobuthus weneri</i>	0.230	0.208	0.236	0.188	0.192	0.186	0.186	0.190
75	KY982184.1 <i>Centruroides schmidt</i>	0.208	0.200	0.208	0.118	0.118	0.114	0.116	0.116
76	KY982185.1 <i>Centruroides vittatus</i>	0.196	0.192	0.192	0.026	0.026	0.030	0.028	0.008
77	KY982187.1 <i>Heteroctenus abudi</i>	0.204	0.210	0.198	0.148	0.154	0.148	0.150	0.146
78	KY982188.1 <i>Heteroctenus abudi</i>	0.198	0.202	0.200	0.138	0.144	0.138	0.140	0.136
79	KY982192.1 <i>Heteroctenus junceus</i>	0.214	0.202	0.210	0.126	0.132	0.126	0.124	0.138
80	KY982193.1 <i>Heteroctenus junceus</i>	0.216	0.202	0.208	0.126	0.132	0.126	0.124	0.138
81	KY982194.1 <i>Heteroctenus junceus</i>	0.220	0.204	0.200	0.122	0.128	0.118	0.120	0.134
82	KY982199.1 <i>Heteroctenus junceus</i>	0.210	0.192	0.194	0.114	0.118	0.114	0.112	0.120
83	KY982273.1 <i>Zabius fuscus</i>	0.224	0.218	0.210	0.166	0.168	0.170	0.168	0.162
84	MF422313.1 <i>Isometrus</i> sp.	0.248	0.224	0.214	0.178	0.182	0.182	0.180	0.182
85	MF422319.1 <i>Lychas tricarinatus</i>	0.210	0.210	0.204	0.166	0.170	0.164	0.164	0.170
86	MF422320.1 <i>Lychas tricarinatus</i>	0.208	0.206	0.204	0.168	0.172	0.166	0.166	0.172
87	MF422321.1 <i>Lychas tricarinatus</i>	0.204	0.204	0.200	0.164	0.168	0.162	0.162	0.168
88	MF422322.1 <i>Lychas tricarinatus</i>	0.208	0.206	0.204	0.168	0.172	0.166	0.166	0.172
89	MF422326.1 <i>Lychas tricarinatus</i>	0.218	0.208	0.204	0.152	0.160	0.150	0.150	0.152
90	MF422327.1 <i>Lychas tricarinatus</i>	0.220	0.206	0.198	0.138	0.146	0.136	0.136	0.142
91	MF422328.1 <i>Lychas tricarinatus</i>	0.220	0.200	0.200	0.144	0.152	0.142	0.142	0.146
92	MF422329.1 <i>Lychas tricarinatus</i>	0.220	0.208	0.200	0.140	0.148	0.138	0.138	0.144
93	MF422330.1 <i>Lychas tricarinatus</i>	0.220	0.206	0.198	0.138	0.146	0.136	0.136	0.142
94	MK479161.1 <i>Centruroides arctimanus</i>	0.220	0.190	0.208	0.140	0.138	0.136	0.138	0.134
95	MK479165.1 <i>Centruroides barbudensis</i>	0.208	0.188	0.196	0.128	0.128	0.128	0.126	0.130
96	MK479171.1 <i>Centruroides exilimanus</i>	0.214	0.204	0.206	0.118	0.116	0.116	0.116	0.120
97	MK479180.1 <i>Centruroides insulanus</i>	0.200	0.182	0.190	0.122	0.124	0.120	0.120	0.118
98	MK479188.1 <i>Centruroides morenoi</i>	0.196	0.204	0.206	0.102	0.110	0.100	0.100	0.112
99	MK479196.1 <i>Centruroides platnicki</i>	0.206	0.196	0.202	0.120	0.122	0.120	0.122	0.126
100	MK479202.1 <i>Centruroides simplex</i>	0.200	0.200	0.202	0.100	0.102	0.098	0.098	0.106
101	MK479204.1 <i>Centruroides taino</i>	0.200	0.196	0.206	0.130	0.128	0.126	0.128	0.138
102	MK479207.1 <i>Centruroides testaceus</i>	0.196	0.194	0.208	0.108	0.110	0.106	0.106	0.108
103	MK479210.1 <i>Centruroides vittatus</i>	0.200	0.196	0.192	0.032	0.032	0.036	0.034	0.002
104	NC 037222.1 <i>Centruroides vittatus</i>	0.200	0.196	0.192	0.032	0.032	0.036	0.034	0.002
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.176	0.168	0.188	0.208	0.210	0.206	0.206	0.214
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.214	0.214	0.204	0.198	0.208	0.196	0.196	0.198
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.192	0.184	0.190	0.228	0.232	0.230	0.228	0.228
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.174	0.174	0.146	0.186	0.186	0.188	0.188	0.192

		65	66	67	68	69	70	71	72
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.019	0.018	0.018	0.017	0.018	0.018	0.018
38	KT446946.1 <i>Brachistosternus chango</i>	0.018	0.018	0.017	0.018	0.017	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.019	0.018	0.018	0.018	0.018	0.018	0.018	0.018
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.018	0.018	0.018	0.017	0.017	0.018	0.018	0.018
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.019	0.018	0.018	0.018	0.018	0.018	0.018	0.018
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.019	0.018	0.018	0.018	0.018	0.018	0.018	0.019
43	KX517244.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.018	0.019	0.018	0.018	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.017	0.018	0.018	0.018	0.018
46	KT446986.1 <i>Brachistosternus negrei</i>	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.018	0.018	0.017	0.018	0.018	0.018	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.018	0.018	0.018	0.018	0.018	0.019	0.018	0.018
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.017
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.019	0.019	0.019	0.018	0.018	0.018	0.019	0.018
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.018	0.019	0.018	0.018	0.018	0.018	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.018	0.018	0.018	0.019	0.018	0.019	0.019	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.018	0.018	0.017	0.018	0.018	0.018	0.018	0.019
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.018	0.017	0.018	0.018	0.017	0.017	0.018	0.018
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.019	0.018	0.018	0.019	0.019	0.018	0.019	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.018	0.019	0.018	0.018	0.018	0.018	0.018	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.018	0.018	0.018	0.019	0.018	0.019	0.019	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.017	0.016	0.017	0.017	0.017	0.018	0.016	0.017
61	EF122608.2 <i>Centruroides vittatus</i>	0.017	0.017	0.017	0.017	0.016	0.018	0.017	0.017
62	EF122612.2 <i>Centruroides vittatus</i>	0.017	0.016	0.017	0.017	0.017	0.018	0.016	0.017
63	EU381064.1 <i>Centruroides vittatus</i>	0.017	0.016	0.017	0.017	0.017	0.018	0.016	0.017
64	EU404114.1 <i>Centruroides vittatus</i>	0.017	0.017	0.017	0.017	0.017	0.018	0.016	0.017
65	HM567381.1 <i>Mesobuthus eupeus</i>		0.015	0.016	0.018	0.017	0.017	0.014	0.016
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.128		0.017	0.017	0.017	0.018	0.015	0.017
67	JN018153.1 <i>Lychas mucronatus</i>	0.158	0.174		0.016	0.016	0.013	0.016	0.017
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.194	0.188	0.154		0.018	0.016	0.017	0.017
69	JN018210.1 <i>Lychas mucronatus</i>	0.178	0.184	0.156	0.194		0.017	0.017	0.016
70	JN018211.1 <i>Lychas mucronatus</i>	0.186	0.202	0.088	0.162	0.172		0.017	0.016
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.116	0.122	0.152	0.176	0.182	0.166		0.017
72	KT716037.1 <i>Lychas tricarinatus</i>	0.142	0.182	0.168	0.174	0.158	0.160	0.186	

		65	66	67	68	69	70	71	72
73	KX648425.1 <i>Hottentotta minax</i>	0.138	0.152	0.176	0.176	0.202	0.174	0.136	0.182
74	KX648429.1 <i>Compsobuthus weneri</i>	0.138	0.152	0.176	0.176	0.202	0.174	0.136	0.182
75	KY982184.1 <i>Centruroides schmidt</i>	0.170	0.172	0.160	0.162	0.166	0.192	0.156	0.160
76	KY982185.1 <i>Centruroides vittatus</i>	0.170	0.166	0.176	0.168	0.166	0.202	0.160	0.164
77	KY982187.1 <i>Heteroctenus abudi</i>	0.148	0.176	0.158	0.164	0.180	0.186	0.152	0.152
78	KY982188.1 <i>Heteroctenus abudi</i>	0.144	0.172	0.154	0.162	0.176	0.178	0.144	0.142
79	KY982192.1 <i>Heteroctenus junceus</i>	0.154	0.168	0.176	0.154	0.178	0.186	0.160	0.162
80	KY982193.1 <i>Heteroctenus junceus</i>	0.152	0.168	0.172	0.158	0.174	0.182	0.160	0.160
81	KY982194.1 <i>Heteroctenus junceus</i>	0.138	0.162	0.166	0.156	0.164	0.192	0.154	0.152
82	KY982199.1 <i>Heteroctenus junceus</i>	0.162	0.170	0.180	0.152	0.166	0.198	0.154	0.150
83	KY982273.1 <i>Zabius fuscus</i>	0.160	0.176	0.164	0.196	0.194	0.182	0.170	0.178
84	MF422313.1 <i>Isometrus</i> sp.	0.174	0.194	0.144	0.178	0.160	0.170	0.186	0.172
85	MF422319.1 <i>Lychas tricarinatus</i>	0.136	0.186	0.162	0.168	0.164	0.150	0.186	0.018
86	MF422320.1 <i>Lychas tricarinatus</i>	0.138	0.184	0.162	0.168	0.166	0.150	0.184	0.016
87	MF422321.1 <i>Lychas tricarinatus</i>	0.134	0.182	0.158	0.168	0.162	0.154	0.182	0.012
88	MF422322.1 <i>Lychas tricarinatus</i>	0.138	0.184	0.162	0.168	0.166	0.150	0.184	0.016
89	MF422326.1 <i>Lychas tricarinatus</i>	0.146	0.186	0.156	0.182	0.160	0.166	0.174	0.076
90	MF422327.1 <i>Lychas tricarinatus</i>	0.136	0.182	0.160	0.174	0.156	0.174	0.172	0.066
91	MF422328.1 <i>Lychas tricarinatus</i>	0.128	0.182	0.154	0.178	0.158	0.178	0.172	0.074
92	MF422329.1 <i>Lychas tricarinatus</i>	0.138	0.182	0.158	0.176	0.158	0.176	0.174	0.068
93	MF422330.1 <i>Lychas tricarinatus</i>	0.136	0.182	0.160	0.174	0.156	0.174	0.172	0.066
94	MK479161.1 <i>Centruroides arctimanus</i>	0.156	0.170	0.168	0.170	0.182	0.190	0.170	0.158
95	MK479165.1 <i>Centruroides barbudensis</i>	0.160	0.178	0.178	0.164	0.178	0.182	0.182	0.154
96	MK479171.1 <i>Centruroides exilimanus</i>	0.172	0.176	0.168	0.176	0.174	0.186	0.162	0.176
97	MK479180.1 <i>Centruroides insulanus</i>	0.148	0.156	0.158	0.146	0.172	0.178	0.144	0.136
98	MK479188.1 <i>Centruroides morenoi</i>	0.152	0.174	0.170	0.162	0.160	0.180	0.152	0.146
99	MK479196.1 <i>Centruroides platnicki</i>	0.170	0.176	0.158	0.166	0.164	0.184	0.166	0.160
100	MK479202.1 <i>Centruroides simplex</i>	0.168	0.164	0.158	0.156	0.160	0.190	0.138	0.148
101	MK479204.1 <i>Centruroides taino</i>	0.160	0.166	0.160	0.150	0.168	0.172	0.156	0.146
102	MK479207.1 <i>Centruroides testaceus</i>	0.178	0.178	0.164	0.142	0.170	0.186	0.150	0.154
103	MK479210.1 <i>Centruroides vittatus</i>	0.170	0.168	0.178	0.176	0.170	0.200	0.162	0.166
104	NC 037222.1 <i>Centruroides vittatus</i>	0.170	0.168	0.178	0.176	0.170	0.200	0.162	0.166
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.208	0.224	0.198	0.202	0.194	0.206	0.230	0.192
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.218	0.228	0.214	0.204	0.220	0.218	0.226	0.208
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.242	0.246	0.192	0.208	0.206	0.206	0.234	0.222
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.206	0.216	0.204	0.208	0.174	0.206	0.212	0.188

		73	74	75	76	77	78	79	80
1	PP07	0.017	0.017	0.016	0.017	0.016	0.016	0.017	0.017
2	PP08	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.017
3	PP11	0.017	0.017	0.016	0.017	0.017	0.016	0.017	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.017	0.017	0.016	0.016	0.016	0.016	0.017	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.018	0.018	0.018	0.018	0.018	0.018	0.017	0.017
7	<i>Lychas annulatus</i> clade B PC04	0.017	0.017	0.016	0.016	0.016	0.017	0.017	0.017
8	<i>Urodacus</i> sp Telfer PC05	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
9	<i>Lychas annulatus</i> clade A PC06	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
11	<i>Urodacus yaschenkoki</i> PC08	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
12	<i>Lychas annulatus</i> clade B NN01	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.017
13	<i>Lychas annulatus</i> clade A NN03	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.017	0.017	0.016	0.017	0.017	0.016	0.017	0.017
15	<i>Lychas annulatus</i> NN05 clade A	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.017	0.017	0.016	0.017	0.017	0.017	0.017	0.017
20	<i>Lychas annulatus</i> clade ANN10	0.016	0.016	0.016	0.017	0.016	0.016	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.017	0.017	0.014	0.007	0.016	0.015	0.015	0.015
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
23	KT446990. <i>Brachistosternus paposo</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.018	0.018
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.017	0.017	0.017	0.018	0.018	0.018
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.017	0.017	0.018	0.018	0.017	0.017
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.019	0.019	0.017	0.017	0.018	0.018	0.018	0.018
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.018	0.018	0.017	0.016	0.017	0.017	0.017	0.017
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
29	KX517230.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.018	0.018
30	KX517229.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.018	0.018
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.018	0.018	0.018	0.018	0.017	0.017	0.018	0.018
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.018	0.018	0.018	0.018	0.017	0.017	0.018	0.018
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.019	0.019	0.017	0.018	0.017	0.017	0.017	0.017
34	AY156581.1 <i>Pandinus dictator</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.018	0.018	0.017	0.018	0.017	0.017	0.017	0.017
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.017	0.017	0.018	0.018	0.018	0.018

		73	74	75	76	77	78	79	80
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.017	0.017	0.018	0.018	0.018	0.018
38	KT446946.1 <i>Brachistosternus chango</i>	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.018	0.018	0.018	0.018	0.018	0.017	0.017	0.017
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.018	0.018	0.017	0.017	0.018	0.018	0.017	0.017
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.019	0.019	0.017	0.017	0.018	0.018	0.018	0.017
43	KX517244.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.017	0.017	0.017	0.018	0.018	0.018
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.017	0.017	0.017	0.018	0.018	0.018
46	KT446986.1 <i>Brachistosternus negrei</i>	0.019	0.019	0.018	0.018	0.017	0.017	0.018	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.017	0.017	0.017	0.018	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.018	0.018	0.017	0.018	0.018	0.018	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.018	0.018	0.018	0.017	0.017	0.017	0.017	0.017
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.017	0.017	0.018	0.018	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.018	0.018	0.018	0.017	0.018	0.018	0.017	0.017
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.018	0.018	0.018	0.017	0.017	0.017	0.018	0.018
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.019	0.019	0.018	0.018	0.018	0.018	0.018	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.017	0.017	0.014	0.007	0.016	0.015	0.015	0.015
61	EF122608.2 <i>Centruroides vittatus</i>	0.018	0.018	0.014	0.007	0.016	0.016	0.015	0.015
62	EF122612.2 <i>Centruroides vittatus</i>	0.017	0.017	0.014	0.008	0.016	0.015	0.015	0.015
63	EU381064.1 <i>Centruroides vittatus</i>	0.017	0.017	0.014	0.007	0.016	0.016	0.015	0.015
64	EU404114.1 <i>Centruroides vittatus</i>	0.018	0.018	0.014	0.004	0.016	0.015	0.015	0.015
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.015	0.015	0.017	0.017	0.016	0.016	0.016	0.016
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
67	JN018153.1 <i>Lychas mucronatus</i>	0.017	0.017	0.016	0.017	0.016	0.016	0.017	0.017
68	JN018154.1 <i>Parabuthus laevisfrons</i>	0.017	0.017	0.016	0.017	0.017	0.016	0.016	0.016
69	JN018210.1 <i>Lychas mucronatus</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
70	JN018211.1 <i>Lychas mucronatus</i>	0.017	0.017	0.018	0.018	0.017	0.017	0.017	0.017
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016
72	KT716037.1 <i>Lychas tricarinatus</i>	0.017	0.017	0.016	0.017	0.016	0.016	0.016	0.016

		73	74	75	76	77	78	79	80
73	KX648425.1 <i>Hottentotta minax</i>		0.000	0.017	0.017	0.017	0.017	0.017	0.017
74	KX648429.1 <i>Compsobuthus weneri</i>	0.000		0.017	0.017	0.017	0.017	0.017	0.017
75	KY982184.1 <i>Centruroides schmidt</i>	0.178	0.178		0.014	0.014	0.014	0.014	0.014
76	KY982185.1 <i>Centruroides vittatus</i>	0.188	0.188	0.110		0.016	0.015	0.015	0.015
77	KY982187.1 <i>Heteroctenus abudi</i>	0.180	0.180	0.116	0.146		0.004	0.014	0.014
78	KY982188.1 <i>Heteroctenus abudi</i>	0.174	0.174	0.116	0.136	0.010		0.014	0.014
79	KY982192.1 <i>Heteroctenus junceus</i>	0.180	0.180	0.118	0.134	0.118	0.116		0.003
80	KY982193.1 <i>Heteroctenus junceus</i>	0.176	0.176	0.114	0.134	0.114	0.112	0.004	
81	KY982194.1 <i>Heteroctenus junceus</i>	0.174	0.174	0.112	0.132	0.098	0.098	0.046	0.042
82	KY982199.1 <i>Heteroctenus junceus</i>	0.176	0.176	0.122	0.114	0.120	0.118	0.058	0.058
83	KY982273.1 <i>Zabius fuscus</i>	0.182	0.182	0.160	0.160	0.150	0.152	0.150	0.148
84	MF422313.1 <i>Isometrus</i> sp.	0.172	0.172	0.180	0.178	0.174	0.180	0.176	0.176
85	MF422319.1 <i>Lychas tricarinatus</i>	0.180	0.180	0.166	0.166	0.154	0.144	0.166	0.164
86	MF422320.1 <i>Lychas tricarinatus</i>	0.180	0.180	0.164	0.168	0.152	0.142	0.166	0.164
87	MF422321.1 <i>Lychas tricarinatus</i>	0.178	0.178	0.160	0.164	0.148	0.138	0.162	0.160
88	MF422322.1 <i>Lychas tricarinatus</i>	0.180	0.180	0.164	0.168	0.152	0.142	0.166	0.164
89	MF422326.1 <i>Lychas tricarinatus</i>	0.180	0.180	0.160	0.148	0.162	0.156	0.172	0.170
90	MF422327.1 <i>Lychas tricarinatus</i>	0.170	0.170	0.148	0.138	0.156	0.146	0.166	0.164
91	MF422328.1 <i>Lychas tricarinatus</i>	0.178	0.178	0.158	0.142	0.162	0.152	0.164	0.162
92	MF422329.1 <i>Lychas tricarinatus</i>	0.170	0.170	0.146	0.140	0.156	0.146	0.168	0.166
93	MF422330.1 <i>Lychas tricarinatus</i>	0.170	0.170	0.148	0.138	0.156	0.146	0.166	0.164
94	MK479161.1 <i>Centruroides arctimanus</i>	0.174	0.174	0.108	0.128	0.130	0.126	0.114	0.114
95	MK479165.1 <i>Centruroides barbudensis</i>	0.174	0.174	0.126	0.130	0.126	0.120	0.120	0.120
96	MK479171.1 <i>Centruroides exilimanus</i>	0.188	0.188	0.134	0.114	0.140	0.136	0.130	0.130
97	MK479180.1 <i>Centruroides insulanus</i>	0.164	0.164	0.098	0.116	0.116	0.108	0.122	0.118
98	MK479188.1 <i>Centruroides morenoi</i>	0.184	0.184	0.110	0.110	0.124	0.118	0.108	0.108
99	MK479196.1 <i>Centruroides platnicki</i>	0.182	0.182	0.104	0.122	0.122	0.116	0.116	0.116
100	MK479202.1 <i>Centruroides simplex</i>	0.170	0.170	0.102	0.100	0.134	0.128	0.120	0.120
101	MK479204.1 <i>Centruroides taino</i>	0.180	0.180	0.122	0.136	0.124	0.118	0.116	0.116
102	MK479207.1 <i>Centruroides testaceus</i>	0.172	0.172	0.100	0.102	0.136	0.134	0.124	0.124
103	MK479210.1 <i>Centruroides vittatus</i>	0.188	0.188	0.118	0.010	0.148	0.138	0.140	0.140
104	NC 037222.1 <i>Centruroides vittatus</i>	0.188	0.188	0.118	0.010	0.148	0.138	0.140	0.140
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.222	0.222	0.194	0.212	0.198	0.202	0.220	0.216
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.206	0.206	0.202	0.194	0.214	0.212	0.202	0.200
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.238	0.238	0.220	0.228	0.226	0.224	0.228	0.224
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.226	0.226	0.202	0.190	0.204	0.204	0.198	0.194

		81	82	83	84	85	86	87	88
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
38	KT446946.1 <i>Brachistosternus chango</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.018	0.019	0.018	0.019	0.019	0.019	0.019	0.019
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.018
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.017	0.017	0.018	0.018	0.018	0.018	0.018	0.018
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.018	0.017	0.018	0.019	0.019	0.019	0.019	0.019
43	KX517244.1 <i>Brachistosternus paposo</i>	0.018	0.017	0.018	0.018	0.018	0.018	0.018	0.018
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.018	0.017	0.018	0.019	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.018	0.017	0.018	0.018	0.018	0.018	0.018	0.018
46	KT446986.1 <i>Brachistosternus negrei</i>	0.018	0.018	0.018	0.019	0.018	0.018	0.017	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.018	0.018	0.018	0.018	0.018	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.017	0.017	0.017	0.018	0.018	0.018	0.018	0.018
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.017	0.017	0.018	0.018	0.018	0.018	0.018	0.018
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.018	0.017	0.018	0.018	0.018	0.018	0.018	0.018
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.018	0.018	0.019	0.019	0.018	0.018	0.018	0.018
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.017	0.017	0.018	0.018	0.019	0.019	0.019	0.019
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.017	0.017	0.019	0.018	0.018	0.018	0.018	0.018
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.019	0.018	0.019	0.019	0.018	0.018	0.018	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.018	0.018	0.018	0.019	0.018	0.018	0.018	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.015	0.014	0.017	0.017	0.017	0.017	0.017	0.017
61	EF122608.2 <i>Centruroides vittatus</i>	0.015	0.014	0.017	0.017	0.017	0.017	0.017	0.017
62	EF122612.2 <i>Centruroides vittatus</i>	0.014	0.014	0.017	0.017	0.017	0.017	0.016	0.017
63	EU381064.1 <i>Centruroides vittatus</i>	0.015	0.014	0.017	0.017	0.017	0.017	0.016	0.017
64	EU404114.1 <i>Centruroides vittatus</i>	0.015	0.015	0.016	0.017	0.017	0.017	0.017	0.017
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.015	0.016	0.016	0.017	0.015	0.015	0.015	0.015
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.016	0.017	0.017	0.018	0.017	0.017	0.017	0.017
67	JN018153.1 <i>Lychas mucronatus</i>	0.017	0.017	0.017	0.016	0.016	0.016	0.016	0.016
68	JN018154.1 <i>Parabuthus laevisfrons</i>	0.016	0.016	0.018	0.017	0.017	0.017	0.017	0.017
69	JN018210.1 <i>Lychas mucronatus</i>	0.017	0.017	0.018	0.016	0.017	0.017	0.016	0.017
70	JN018211.1 <i>Lychas mucronatus</i>	0.018	0.018	0.017	0.017	0.016	0.016	0.016	0.016
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.016	0.016	0.017	0.017	0.017	0.017	0.017	0.017
72	KT716037.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.017	0.017	0.006	0.006	0.005	0.006

		81	82	83	84	85	86	87	88
73	KX648425.1 <i>Hottentotta minax</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
74	KX648429.1 <i>Compsobuthus weneri</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
75	KY982184.1 <i>Centruroides schmidt</i>	0.014	0.015	0.016	0.017	0.017	0.017	0.016	0.017
76	KY982185.1 <i>Centruroides vittatus</i>	0.015	0.014	0.016	0.017	0.017	0.017	0.017	0.017
77	KY982187.1 <i>Heteroctenus abudi</i>	0.013	0.015	0.016	0.017	0.016	0.016	0.016	0.016
78	KY982188.1 <i>Heteroctenus abudi</i>	0.013	0.014	0.016	0.017	0.016	0.016	0.015	0.016
79	KY982192.1 <i>Heteroctenus junceus</i>	0.009	0.010	0.016	0.017	0.017	0.017	0.016	0.017
80	KY982193.1 <i>Heteroctenus junceus</i>	0.009	0.010	0.016	0.017	0.017	0.017	0.016	0.017
81	KY982194.1 <i>Heteroctenus junceus</i>		0.010	0.016	0.017	0.016	0.016	0.016	0.016
82	KY982199.1 <i>Heteroctenus junceus</i>	0.054		0.016	0.017	0.016	0.016	0.016	0.016
83	KY982273.1 <i>Zabius fuscus</i>	0.156	0.160		0.018	0.017	0.017	0.017	0.017
84	MF422313.1 <i>Isometrus</i> sp.	0.176	0.180	0.190		0.016	0.016	0.017	0.016
85	MF422319.1 <i>Lychas tricarinatus</i>	0.152	0.158	0.182	0.162		0.003	0.003	0.003
86	MF422320.1 <i>Lychas tricarinatus</i>	0.156	0.158	0.180	0.162	0.006		0.003	0.000
87	MF422321.1 <i>Lychas tricarinatus</i>	0.152	0.154	0.176	0.164	0.006	0.004		0.003
88	MF422322.1 <i>Lychas tricarinatus</i>	0.156	0.158	0.180	0.162	0.006	0.000	0.004	
89	MF422326.1 <i>Lychas tricarinatus</i>	0.162	0.172	0.174	0.162	0.074	0.068	0.072	0.068
90	MF422327.1 <i>Lychas tricarinatus</i>	0.158	0.162	0.176	0.160	0.064	0.062	0.058	0.062
91	MF422328.1 <i>Lychas tricarinatus</i>	0.156	0.174	0.166	0.168	0.072	0.074	0.070	0.074
92	MF422329.1 <i>Lychas tricarinatus</i>	0.160	0.164	0.176	0.160	0.066	0.064	0.060	0.064
93	MF422330.1 <i>Lychas tricarinatus</i>	0.158	0.162	0.176	0.160	0.064	0.062	0.058	0.062
94	MK479161.1 <i>Centruroides arctimanus</i>	0.114	0.114	0.158	0.164	0.162	0.160	0.158	0.160
95	MK479165.1 <i>Centruroides barbudensis</i>	0.122	0.118	0.152	0.178	0.152	0.148	0.150	0.148
96	MK479171.1 <i>Centruroides exilimanus</i>	0.130	0.124	0.154	0.166	0.176	0.174	0.172	0.174
97	MK479180.1 <i>Centruroides insulanus</i>	0.108	0.112	0.160	0.176	0.144	0.142	0.140	0.142
98	MK479188.1 <i>Centruroides morenoi</i>	0.100	0.114	0.176	0.182	0.144	0.144	0.142	0.144
99	MK479196.1 <i>Centruroides platnicki</i>	0.112	0.110	0.148	0.172	0.162	0.164	0.160	0.164
100	MK479202.1 <i>Centruroides simplex</i>	0.110	0.104	0.180	0.170	0.150	0.152	0.148	0.152
101	MK479204.1 <i>Centruroides taino</i>	0.102	0.114	0.162	0.178	0.140	0.140	0.138	0.140
102	MK479207.1 <i>Centruroides testaceus</i>	0.122	0.106	0.164	0.184	0.152	0.150	0.146	0.150
103	MK479210.1 <i>Centruroides vittatus</i>	0.136	0.122	0.164	0.180	0.168	0.170	0.166	0.170
104	NC 037222.1 <i>Centruroides vittatus</i>	0.136	0.122	0.164	0.180	0.168	0.170	0.166	0.170
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.202	0.220	0.232	0.206	0.188	0.190	0.186	0.190
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.202	0.190	0.198	0.214	0.206	0.204	0.206	0.204
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.222	0.230	0.220	0.204	0.218	0.220	0.220	0.220
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.196	0.188	0.200	0.210	0.198	0.198	0.194	0.198

		89	90	91	92	93	94	95	96
1	PP07	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
2	PP08	0.015	0.016	0.016	0.016	0.016	0.017	0.017	0.017
3	PP11	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.018	0.017	0.018	0.017	0.017	0.018	0.018	0.017
7	<i>Lychas annulatus</i> clade B PC04	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
8	<i>Urodacus</i> sp Telfer PC05	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
9	<i>Lychas annulatus</i> clade A PC06	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
11	<i>Urodacus yaschenkoki</i> PC08	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
12	<i>Lychas annulatus</i> clade B NN01	0.016	0.016	0.017	0.016	0.016	0.017	0.017	0.017
13	<i>Lychas annulatus</i> clade A NN03	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
15	<i>Lychas annulatus</i> NN05 clade A	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
20	<i>Lychas annulatus</i> clade ANN10	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.016	0.015	0.016	0.016	0.015	0.016	0.015	0.014
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
23	KT446990. <i>Brachistosternus paposo</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.017
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.018	0.017	0.018	0.018	0.017	0.017
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.019	0.018	0.019	0.018	0.018	0.018	0.018	0.018
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.018	0.018	0.018	0.018	0.018	0.017	0.017	0.017
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.018	0.018	0.017	0.018	0.018	0.018	0.018	0.018
29	KX517230.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
30	KX517229.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
34	AY156581.1 <i>Pandinus dictator</i>	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.017
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.018

		89	90	91	92	93	94	95	96
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
38	KT446946.1 <i>Brachistosternus chango</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.019	0.019	0.019	0.019	0.019	0.018	0.019	0.018
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.018	0.018	0.018	0.018	0.018	0.018	0.017	0.017
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.018	0.018	0.018	0.018	0.018	0.017	0.017	0.017
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.019	0.019	0.019	0.019	0.019	0.018	0.018	0.018
43	KX517244.1 <i>Brachistosternus paposo</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.017
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
46	KT446986.1 <i>Brachistosternus negrei</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.018	0.018	0.018	0.018	0.018	0.017	0.018	0.018
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.018	0.017	0.017	0.017	0.017	0.018	0.018	0.018
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.017
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.019	0.018	0.019	0.019	0.018	0.018	0.018	0.019
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.018	0.019	0.018	0.019	0.019	0.018	0.018	0.018
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.018	0.019	0.019	0.019	0.019	0.019	0.018	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.018	0.018	0.018	0.018	0.018	0.018	0.017	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.016	0.015	0.016	0.016	0.015	0.016	0.015	0.014
61	EF122608.2 <i>Centruroides vittatus</i>	0.016	0.016	0.016	0.016	0.016	0.015	0.015	0.014
62	EF122612.2 <i>Centruroides vittatus</i>	0.016	0.015	0.016	0.015	0.015	0.015	0.015	0.014
63	EU381064.1 <i>Centruroides vittatus</i>	0.016	0.015	0.016	0.015	0.015	0.015	0.015	0.014
64	EU404114.1 <i>Centruroides vittatus</i>	0.016	0.016	0.016	0.016	0.016	0.015	0.015	0.015
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.016	0.015	0.015	0.015	0.015	0.016	0.016	0.017
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
67	JN018153.1 <i>Lychas mucronatus</i>	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
69	JN018210.1 <i>Lychas mucronatus</i>	0.016	0.016	0.016	0.016	0.016	0.017	0.017	0.017
70	JN018211.1 <i>Lychas mucronatus</i>	0.017	0.017	0.017	0.017	0.017	0.018	0.017	0.017
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.016
72	KT716037.1 <i>Lychas tricarinatus</i>	0.012	0.011	0.012	0.011	0.011	0.016	0.016	0.017

		89	90	91	92	93	94	95	96
73	KX648425.1 <i>Hottentotta minax</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
74	KX648429.1 <i>Compsobuthus weneri</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
75	KY982184.1 <i>Centruroides schmidt</i>	0.016	0.016	0.016	0.016	0.016	0.014	0.015	0.015
76	KY982185.1 <i>Centruroides vittatus</i>	0.016	0.015	0.016	0.016	0.015	0.015	0.015	0.014
77	KY982187.1 <i>Heteroctenus abudi</i>	0.016	0.016	0.016	0.016	0.016	0.015	0.015	0.016
78	KY982188.1 <i>Heteroctenus abudi</i>	0.016	0.016	0.016	0.016	0.016	0.015	0.015	0.015
79	KY982192.1 <i>Heteroctenus junceus</i>	0.017	0.017	0.017	0.017	0.017	0.014	0.015	0.015
80	KY982193.1 <i>Heteroctenus junceus</i>	0.017	0.017	0.016	0.017	0.017	0.014	0.015	0.015
81	KY982194.1 <i>Heteroctenus junceus</i>	0.016	0.016	0.016	0.016	0.016	0.014	0.015	0.015
82	KY982199.1 <i>Heteroctenus junceus</i>	0.017	0.016	0.017	0.017	0.016	0.014	0.014	0.015
83	KY982273.1 <i>Zabius fuscus</i>	0.017	0.017	0.017	0.017	0.017	0.016	0.016	0.016
84	MF422313.1 <i>Isometrus</i> sp.	0.016	0.016	0.017	0.016	0.016	0.017	0.017	0.017
85	MF422319.1 <i>Lychas tricarinatus</i>	0.012	0.011	0.012	0.011	0.011	0.016	0.016	0.017
86	MF422320.1 <i>Lychas tricarinatus</i>	0.011	0.011	0.012	0.011	0.011	0.016	0.016	0.017
87	MF422321.1 <i>Lychas tricarinatus</i>	0.012	0.010	0.011	0.011	0.010	0.016	0.016	0.017
88	MF422322.1 <i>Lychas tricarinatus</i>	0.011	0.011	0.012	0.011	0.011	0.016	0.016	0.017
89	MF422326.1 <i>Lychas tricarinatus</i>		0.010	0.009	0.010	0.010	0.016	0.016	0.017
90	MF422327.1 <i>Lychas tricarinatus</i>	0.048		0.009	0.002	0.000	0.016	0.016	0.017
91	MF422328.1 <i>Lychas tricarinatus</i>	0.042	0.038		0.009	0.009	0.016	0.016	0.017
92	MF422329.1 <i>Lychas tricarinatus</i>	0.050	0.002	0.040		0.002	0.016	0.016	0.017
93	MF422330.1 <i>Lychas tricarinatus</i>	0.048	0.000	0.038	0.002		0.016	0.016	0.017
94	MK479161.1 <i>Centruroides arctimanus</i>	0.158	0.156	0.150	0.156	0.156		0.014	0.015
95	MK479165.1 <i>Centruroides barbudensis</i>	0.158	0.150	0.152	0.152	0.150	0.112		0.016
96	MK479171.1 <i>Centruroides exilimanus</i>	0.174	0.170	0.178	0.172	0.170	0.122	0.140	
97	MK479180.1 <i>Centruroides insulanus</i>	0.142	0.136	0.134	0.138	0.136	0.090	0.110	0.116
98	MK479188.1 <i>Centruroides morenoi</i>	0.146	0.138	0.142	0.140	0.138	0.116	0.102	0.118
99	MK479196.1 <i>Centruroides platnicki</i>	0.162	0.156	0.154	0.158	0.156	0.102	0.100	0.136
100	MK479202.1 <i>Centruroides simplex</i>	0.146	0.150	0.152	0.152	0.150	0.124	0.134	0.106
101	MK479204.1 <i>Centruroides taino</i>	0.162	0.154	0.158	0.156	0.154	0.116	0.100	0.142
102	MK479207.1 <i>Centruroides testaceus</i>	0.142	0.148	0.150	0.150	0.148	0.126	0.124	0.108
103	MK479210.1 <i>Centruroides vittatus</i>	0.150	0.140	0.144	0.142	0.140	0.132	0.132	0.118
104	NC 037222.1 <i>Centruroides vittatus</i>	0.150	0.140	0.144	0.142	0.140	0.132	0.132	0.118
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.218	0.204	0.206	0.206	0.204	0.206	0.220	0.216
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.208	0.212	0.218	0.212	0.212	0.208	0.210	0.206
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.224	0.232	0.228	0.230	0.232	0.228	0.236	0.228
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.206	0.208	0.206	0.210	0.208	0.206	0.216	0.188

		97	98	99	100	101	102	103	104
1	PP07	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
2	PP08	0.016	0.017	0.016	0.016	0.016	0.017	0.017	0.017
3	PP11	0.017	0.017	0.016	0.016	0.016	0.016	0.017	0.017
4	<i>Lychas annulatus</i> clade B PC01	0.017	0.017	0.016	0.016	0.016	0.016	0.016	0.016
5	<i>Lychas annulatus</i> clade A PC02	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
6	<i>Urodacus varians</i> PC03	0.017	0.018	0.017	0.018	0.017	0.017	0.018	0.018
7	<i>Lychas annulatus</i> clade B PC04	0.017	0.017	0.016	0.016	0.016	0.016	0.016	0.016
8	<i>Urodacus</i> sp Telfer PC05	0.018	0.017	0.018	0.017	0.018	0.017	0.018	0.018
9	<i>Lychas annulatus</i> clade A PC06	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.017	0.018	0.018	0.017	0.017	0.017	0.018	0.018
11	<i>Urodacus yaschenkoki</i> PC08	0.017	0.018	0.018	0.017	0.017	0.017	0.018	0.018
12	<i>Lychas annulatus</i> clade B NN01	0.017	0.017	0.017	0.016	0.016	0.016	0.017	0.017
13	<i>Lychas annulatus</i> clade A NN03	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.017	0.017	0.017	0.016	0.016	0.016	0.017	0.017
15	<i>Lychas annulatus</i> NN05 clade A	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.017	0.017	0.017	0.016	0.016	0.016	0.017	0.017
20	<i>Lychas annulatus</i> clade ANN10	0.016	0.017	0.016	0.016	0.016	0.016	0.017	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.015	0.014	0.015	0.013	0.015	0.014	0.008	0.008
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.017	0.018	0.018	0.017	0.018	0.017	0.018	0.018
23	KT446990. <i>Brachistosternus paposo</i>	0.018	0.017	0.017	0.017	0.017	0.017	0.017	0.017
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.018	0.018
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.017	0.017	0.017	0.017	0.018	0.017	0.018	0.018
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.017	0.017	0.017	0.017	0.016	0.017	0.017	0.017
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.017	0.017	0.018	0.017	0.017	0.017	0.018	0.018
29	KX517230.1 <i>Brachistosternus paposo</i>	0.018	0.017	0.017	0.017	0.017	0.017	0.017	0.017
30	KX517229.1 <i>Brachistosternus paposo</i>	0.018	0.017	0.017	0.017	0.017	0.017	0.017	0.017
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.017	0.018	0.018	0.018	0.018	0.018	0.018	0.018
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.017	0.017	0.018	0.017	0.018	0.018	0.018	0.018
34	AY156581.1 <i>Pandinus dictator</i>	0.016	0.017	0.017	0.016	0.017	0.016	0.017	0.017
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.018	0.017	0.017	0.017	0.018	0.017	0.017	0.017

		97	98	99	100	101	102	103	104
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.018	0.018	0.017	0.017	0.017	0.017	0.017	0.017
38	KT446946.1 <i>Brachistosternus chango</i>	0.017	0.017	0.017	0.018	0.017	0.018	0.018	0.018
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.017	0.018	0.017	0.017	0.018	0.017	0.018	0.018
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.017	0.016	0.017	0.017	0.018	0.017	0.017	0.017
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.017	0.018	0.018	0.017	0.018	0.017	0.018	0.018
43	KX517244.1 <i>Brachistosternus paposo</i>	0.018	0.017	0.017	0.017	0.018	0.017	0.017	0.017
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.018	0.018	0.018	0.017	0.018	0.018	0.018	0.018
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
46	KT446986.1 <i>Brachistosternus negrei</i>	0.017	0.018	0.017	0.018	0.018	0.018	0.018	0.018
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.017	0.018	0.017	0.017	0.017	0.017	0.018	0.018
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.018	0.018	0.018	0.018	0.017	0.017	0.018	0.018
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.017	0.018	0.017	0.017	0.017	0.018	0.017	0.017
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.017	0.017	0.017	0.017	0.017	0.017	0.018	0.018
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.018	0.018	0.018	0.019	0.018	0.018	0.018	0.018
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.018	0.017	0.017	0.017	0.017	0.017	0.018	0.018
54	KT188365.1 <i>Scorpio palmatus</i>	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.018	0.018	0.017	0.018	0.017	0.017	0.018	0.018
56	JQ514248. <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.017	0.017	0.018	0.017	0.017	0.017	0.017	0.017
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.017	0.018	0.018	0.018	0.018	0.018	0.018	0.018
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
60	EF122607.2 <i>Centruroides vittatus</i>	0.015	0.014	0.015	0.013	0.015	0.014	0.008	0.008
61	EF122608.2 <i>Centruroides vittatus</i>	0.015	0.014	0.015	0.014	0.015	0.014	0.008	0.008
62	EF122612.2 <i>Centruroides vittatus</i>	0.015	0.013	0.015	0.013	0.015	0.014	0.008	0.008
63	EU381064.1 <i>Centruroides vittatus</i>	0.015	0.013	0.015	0.013	0.015	0.014	0.008	0.008
64	EU404114.1 <i>Centruroides vittatus</i>	0.014	0.014	0.015	0.014	0.015	0.014	0.002	0.002
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.016	0.016	0.017	0.017	0.016	0.017	0.017	0.017
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.016	0.017	0.017	0.017	0.017	0.017	0.017	0.017
67	JN018153.1 <i>Lychas mucronatus</i>	0.016	0.017	0.016	0.016	0.016	0.017	0.017	0.017
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.017
69	JN018210.1 <i>Lychas mucronatus</i>	0.017	0.016	0.017	0.016	0.017	0.017	0.017	0.017
70	JN018211.1 <i>Lychas mucronatus</i>	0.017	0.017	0.017	0.018	0.017	0.017	0.018	0.018
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.016	0.016	0.017	0.015	0.016	0.016	0.016	0.016
72	KT716037.1 <i>Lychas tricarinatus</i>	0.015	0.016	0.016	0.016	0.016	0.016	0.017	0.017

		97	98	99	100	101	102	103	104
73	KX648425.1 <i>Hottentotta minax</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
74	KX648429.1 <i>Compsobuthus weneri</i>	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
75	KY982184.1 <i>Centruroides schmidt</i>	0.013	0.014	0.014	0.014	0.015	0.013	0.014	0.014
76	KY982185.1 <i>Centruroides vittatus</i>	0.014	0.014	0.015	0.013	0.015	0.014	0.004	0.004
77	KY982187.1 <i>Heteroctenus abudi</i>	0.014	0.015	0.015	0.015	0.015	0.015	0.016	0.016
78	KY982188.1 <i>Heteroctenus abudi</i>	0.014	0.014	0.014	0.015	0.014	0.015	0.015	0.015
79	KY982192.1 <i>Heteroctenus junceus</i>	0.015	0.014	0.014	0.015	0.014	0.015	0.016	0.016
80	KY982193.1 <i>Heteroctenus junceus</i>	0.014	0.014	0.014	0.015	0.014	0.015	0.016	0.016
81	KY982194.1 <i>Heteroctenus junceus</i>	0.014	0.013	0.014	0.014	0.014	0.015	0.015	0.015
82	KY982199.1 <i>Heteroctenus junceus</i>	0.014	0.014	0.014	0.014	0.014	0.014	0.015	0.015
83	KY982273.1 <i>Zabius fuscus</i>	0.016	0.017	0.016	0.017	0.016	0.017	0.017	0.017
84	MF422313.1 <i>Isometrus</i> sp.	0.017	0.017	0.017	0.017	0.017	0.017	0.017	0.017
85	MF422319.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.016	0.016	0.016	0.016	0.017	0.017
86	MF422320.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.017
87	MF422321.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.016	0.016	0.015	0.016	0.017	0.017
88	MF422322.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.017	0.016	0.016	0.016	0.017	0.017
89	MF422326.1 <i>Lychas tricarinatus</i>	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016
90	MF422327.1 <i>Lychas tricarinatus</i>	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016
91	MF422328.1 <i>Lychas tricarinatus</i>	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
92	MF422329.1 <i>Lychas tricarinatus</i>	0.015	0.016	0.016	0.016	0.016	0.016	0.016	0.016
93	MF422330.1 <i>Lychas tricarinatus</i>	0.015	0.015	0.016	0.016	0.016	0.016	0.016	0.016
94	MK479161.1 <i>Centruroides arctimanus</i>	0.013	0.014	0.014	0.015	0.014	0.015	0.015	0.015
95	MK479165.1 <i>Centruroides barbudensis</i>	0.014	0.014	0.013	0.015	0.013	0.015	0.015	0.015
96	MK479171.1 <i>Centruroides exilimanus</i>	0.014	0.014	0.015	0.014	0.016	0.014	0.014	0.014
97	MK479180.1 <i>Centruroides insulanus</i>		0.014	0.014	0.014	0.013	0.015	0.014	0.014
98	MK479188.1 <i>Centruroides morenoi</i>	0.104		0.015	0.013	0.014	0.013	0.014	0.014
99	MK479196.1 <i>Centruroides platnicki</i>	0.110	0.124		0.014	0.012	0.015	0.015	0.015
100	MK479202.1 <i>Centruroides simplex</i>	0.104	0.098	0.116		0.015	0.010	0.014	0.014
101	MK479204.1 <i>Centruroides taino</i>	0.094	0.108	0.074	0.134		0.015	0.016	0.016
102	MK479207.1 <i>Centruroides testaceus</i>	0.122	0.092	0.132	0.056	0.128		0.014	0.014
103	MK479210.1 <i>Centruroides vittatus</i>	0.116	0.114	0.128	0.108	0.140	0.110		0.000
104	NC 037222.1 <i>Centruroides vittatus</i>	0.116	0.114	0.128	0.108	0.140	0.110	0.000	
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29	0.196	0.204	0.216	0.186	0.206	0.194	0.216	0.216
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.204	0.212	0.208	0.182	0.220	0.188	0.200	0.200
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.232	0.228	0.220	0.226	0.230	0.236	0.230	0.230
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.190	0.200	0.190	0.192	0.204	0.190	0.194	0.194

		105	106	107	108
1	PP07	0.018	0.018	0.018	0.018
2	PP08	0.017	0.018	0.018	0.017
3	PP11	0.018	0.018	0.018	0.018
4	<i>Lychas annulatus</i> clade B PC01	0.018	0.018	0.018	0.017
5	<i>Lychas annulatus</i> clade A PC02	0.017	0.018	0.018	0.017
6	<i>Urodacus varians</i> PC03	0.016	0.017	0.017	0.016
7	<i>Lychas annulatus</i> clade B PC04	0.018	0.018	0.018	0.017
8	<i>Urodacus</i> sp Telfer PC05	0.016	0.017	0.017	0.016
9	<i>Lychas annulatus</i> clade A PC06	0.017	0.018	0.018	0.017
10	<i>Urodacus yaschenkoki</i> PC07	0.016	0.017	0.017	0.016
11	<i>Urodacus yaschenkoki</i> PC08	0.016	0.017	0.017	0.016
12	<i>Lychas annulatus</i> clade B NN01	0.018	0.018	0.018	0.018
13	<i>Lychas annulatus</i> clade A NN03	0.017	0.018	0.018	0.017
14	<i>Lychas annulatus</i> clade B NN04	0.018	0.018	0.018	0.018
15	<i>Lychas annulatus</i> NN05 clade A	0.017	0.018	0.018	0.017
16	<i>Lychas annulatus</i> clade A NN06	0.017	0.018	0.018	0.017
17	<i>Lychas annulatus</i> clade A NN07	0.017	0.018	0.018	0.017
18	<i>Lychas annulatus</i> clade A NN08	0.017	0.018	0.018	0.017
19	<i>Lychas annulatus</i> clade B NN09	0.018	0.018	0.018	0.018
20	<i>Lychas annulatus</i> clade ANN10	0.017	0.018	0.018	0.017
21	EF122605.2 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.017
22	KY295225.1 <i>Urodacus planimanus</i> voucher WAM-T129654	0.016	0.017	0.016	0.015
23	KT446990. <i>Brachistosternus paposo</i>	0.016	0.017	0.017	0.016
24	KT447018.1 <i>Brachistosternus roigalsinai</i>	0.016	0.017	0.016	0.017
25	KT446957.1 <i>Brachistosternus ehrenbergii</i>	0.016	0.017	0.016	0.016
26	KM514656.1 <i>Diplocentrus rectimanus</i> voucher AMCC:LP2032	0.018	0.018	0.018	0.017
27	KM514633.1 <i>Didymocentrus krausi</i> voucher AMCC:LP1987	0.016	0.018	0.017	0.016
28	KM514635.1 <i>Kolotl magnus</i> voucher AMCC:LP7029	0.016	0.018	0.017	0.015
29	KX517230.1 <i>Brachistosternus paposo</i>	0.016	0.017	0.017	0.016
30	KX517229.1 <i>Brachistosternus paposo</i>	0.016	0.017	0.017	0.016
31	KT446947.1 <i>Brachistosternus chilensis</i>	0.016	0.018	0.016	0.016
32	KT446928.1 <i>Brachistosternus aconcagua</i>	0.016	0.018	0.016	0.016
33	KM514636.1 <i>Kolotl poncei</i> voucher AMCC:LP7030	0.016	0.018	0.017	0.016
34	AY156581.1 <i>Pandinus dictator</i>	0.017	0.018	0.017	0.016
35	KM514642.1 <i>Diplocentrus cozumel</i> voucher AMCC:LP4102	0.017	0.018	0.017	0.016
36	KT447015.1 <i>Brachistosternus roigalsinai</i>	0.016	0.017	0.017	0.016

		105	106	107	108
37	KT446955.1 <i>Brachistosternus ehrenbergii</i>	0.016	0.017	0.016	0.016
38	KT446946.1 <i>Brachistosternus chango</i>	0.016	0.018	0.016	0.016
39	KM274783.1 <i>Konetontli chamelaensis</i> voucher LP7675	0.016	0.018	0.017	0.017
40	KU755656.1 <i>Brachistosternus</i> sp. 10 LP-2016 voucher AMCC:LP8355	0.017	0.017	0.016	0.016
41	JQ514251.1 <i>Pandinus imperator</i> voucher Sc1050	0.017	0.018	0.018	0.016
42	KM514641.1 <i>Diplocentrus coylei</i> voucher AMCC:LP7031	0.017	0.018	0.017	0.016
43	KX517244.1 <i>Brachistosternus paposo</i>	0.016	0.017	0.017	0.016
44	KU755642.1 <i>Brachistosternus turpuq</i> voucher AMCC:LP8346	0.016	0.017	0.017	0.017
45	KT447016.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.017
46	KT446986.1 <i>Brachistosternus negrei</i>	0.016	0.018	0.016	0.015
47	KT446952.1 <i>Brachistosternus ehrenbergii</i>	0.016	0.018	0.016	0.015
48	JX909544.1 <i>Paruroctonus boreus</i> voucher SKY42/AMNH	0.016	0.018	0.018	0.017
49	KT446960.1 <i>Brachistosternus ferrugineus</i>	0.016	0.018	0.017	0.016
50	KM514634.1 <i>Didymocentrus lesueurii</i> voucher AMCC:LP3638	0.016	0.017	0.017	0.016
51	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.016	0.017	0.017	0.000
52	KT447025.1 <i>Brachistosternus titicaca</i>	0.016	0.018	0.016	0.016
53	KT447014.1 <i>Brachistosternus roigalsinai</i>	0.017	0.017	0.017	0.017
54	KT188365.1 <i>Scorpio palmatus</i>	0.017	0.018	0.018	0.016
55	JQ514255.1 <i>Chactas</i> sp. AVDM-2012 voucher Sc1000	0.017	0.018	0.018	0.016
56	JQ514248.1 <i>Opisthophthalmus boehmi</i> voucher Sc1137	0.017	0.019	0.018	0.016
57	KM274845.1 <i>Paravaejovis spinigerus</i> voucher LP6317	0.017	0.018	0.018	0.017
58	KM274724.1 <i>Smeringurus grandis</i> voucher LP8690	0.017	0.018	0.017	0.017
59	KT188368.1 <i>Scorpio palmatus</i> isolate 12286D	0.017	0.018	0.018	0.016
60	EF122607.2 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.017
61	EF122608.2 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.017
62	EF122612.2 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.017
63	EU381064.1 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.017
64	EU404114.1 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.018
65	HM567381.1 <i>Mesobuthus eupeus</i>	0.018	0.018	0.019	0.018
66	JF700146.1 <i>Mesobuthus martensii</i> voucher AS27MT03	0.019	0.019	0.019	0.018
67	JN018153.1 <i>Lychas mucronatus</i>	0.018	0.018	0.018	0.018
68	JN018154.1 <i>Parabuthus laevifrons</i>	0.018	0.018	0.018	0.018
69	JN018210.1 <i>Lychas mucronatus</i>	0.018	0.019	0.018	0.017
70	JN018211.1 <i>Lychas mucronatus</i>	0.018	0.018	0.018	0.018
71	KF997876.1 <i>Mesobuthus gibbosus</i>	0.019	0.019	0.019	0.018
72	KT716037.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.017

		105	106	107	108
73	KX648425.1 <i>Hottentotta minax</i>	0.019	0.018	0.019	0.019
74	KX648429.1 <i>Compsobuthus weneri</i>	0.019	0.018	0.019	0.019
75	KY982184.1 <i>Centruroides schmidt</i>	0.018	0.018	0.019	0.018
76	KY982185.1 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.018
77	KY982187.1 <i>Heteroctenus abudi</i>	0.018	0.018	0.019	0.018
78	KY982188.1 <i>Heteroctenus abudi</i>	0.018	0.018	0.019	0.018
79	KY982192.1 <i>Heteroctenus junceus</i>	0.019	0.018	0.019	0.018
80	KY982193.1 <i>Heteroctenus junceus</i>	0.018	0.018	0.019	0.018
81	KY982194.1 <i>Heteroctenus junceus</i>	0.018	0.018	0.019	0.018
82	KY982199.1 <i>Heteroctenus junceus</i>	0.019	0.018	0.019	0.017
83	KY982273.1 <i>Zabius fuscus</i>	0.019	0.018	0.019	0.018
84	MF422313.1 <i>Isometrus</i> sp.	0.018	0.018	0.018	0.018
85	MF422319.1 <i>Lychas tricarinatus</i>	0.017	0.018	0.018	0.018
86	MF422320.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
87	MF422321.1 <i>Lychas tricarinatus</i>	0.017	0.018	0.019	0.018
88	MF422322.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
89	MF422326.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
90	MF422327.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
91	MF422328.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
92	MF422329.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
93	MF422330.1 <i>Lychas tricarinatus</i>	0.018	0.018	0.019	0.018
94	MK479161.1 <i>Centruroides arctimanus</i>	0.018	0.018	0.019	0.018
95	MK479165.1 <i>Centruroides barbudensis</i>	0.019	0.018	0.019	0.018
96	MK479171.1 <i>Centruroides exilimanus</i>	0.018	0.018	0.019	0.017
97	MK479180.1 <i>Centruroides insulanus</i>	0.018	0.018	0.019	0.018
98	MK479188.1 <i>Centruroides morenoi</i>	0.018	0.018	0.019	0.018
99	MK479196.1 <i>Centruroides platnicki</i>	0.018	0.018	0.019	0.018
100	MK479202.1 <i>Centruroides simplex</i>	0.017	0.017	0.019	0.018
101	MK479204.1 <i>Centruroides taino</i>	0.018	0.019	0.019	0.018
102	MK479207.1 <i>Centruroides testaceus</i>	0.018	0.017	0.019	0.018
103	MK479210.1 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.018
104	NC 037222.1 <i>Centruroides vittatus</i>	0.018	0.018	0.019	0.018
105	JN018156.1 <i>Belisarius xambeui</i> voucher MNHN-JAD29		0.018	0.016	0.016
106	JN018163.1 <i>Chaerilus juliettae</i> voucher MNHN-JAB32	0.198		0.019	0.017
107	HM418309.1 <i>Iurus kinzelbachi</i> voucher VF-0846-1	0.154	0.224		0.017
108	KF548118.1 <i>Opisthacanthus asper</i> voucher Sc1087	0.162	0.188	0.180	

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Molecular Systematics of the Winu Short- Range Endemic Invertebrates



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ABN 32 133 230 243
Building F, 661 Newcastle Street
Leederville, Western Australia 6007

Job No.: 814

Prepared by: Dr Karen Cullen
Yvette Hitchen
Hayley Newton

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Molecular Systematics of the Winu Short-Range Endemic Invertebrates

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1.0 Executive Summary

Helix Molecular Solutions was engaged by Biota Environmental Sciences to perform DNA extractions, sequencing of the mitochondrial cytochrome oxidase subunit I gene (COI), and analyses of 11 specimens collected during a short-range endemic (SRE) invertebrate fauna survey of the Winu Borefield survey area. A total of 10 mygalomorph spiders from four families (Anamidae, Barychelidae, Halonoproctidae and Idiopidae) and one scorpion (Buthidae) was collected.

The objective of this project was to gain information on the number of potential species and their apparent distributions, based on the molecular genetic data available for comparison.

Mygalomorphae spider specimens belonging to the family Idiopidae were also sequenced for Cytochrome b (CYB), which is needed to provide confident phylogenetic placement in this group. Similarly, scorpion specimens belonging to the family Buthidae were sequenced for variation of the mitochondrial LSU (large ribosomal subunit) 16S rRNA to provide additional phylogenetic context.

Arachnida: Mygalomorphae – family Anamidae, Barychelidae, Halonoproctidae and Idiopidae

The 10 specimens identified as Mygalomorphae were collected from four sampling sites within the survey area. A total of nine samples were successfully sequenced for COI and two Idiopidae specimens were successfully sequenced for CYB. One specimen originally identified as Idiopidae based on morphology was later reassigned to Halonoproctidae following preliminary molecular analysis. Phylogenetic analysis confirmed the specimens represent three Mygalomorphae families: Anamidae (n=6), Halonoproctidae (n=1) and Idiopidae (n=2). An individual Barychelidae specimen originally identified based on morphology failed to sequence for COI.

An overall total of six putative species were detected. Phylogenetic analysis shows that the six specimens of Anamidae represent two new species of *Aname* (*A. sp.* H-N205 and *A. sp.* H-N206) and one new lineage of a previously detected but undescribed species of *Kwonkan* (*K. sp.* H-N197). *Kwonkan sp.* H-N197 is currently known from only two locations approximately 245 km west of the survey area specimens (TP02 and TP05).

One species of Halonoproctidae was detected, being a new lineage of a previously detected species *Conothele sp.* H-C29. This species is currently known from sites approximately 292 km west northwest of the survey area.

Two new species of Idiopidae (*Idiosoma sp.* H-I90 and *I. sp.* H-I91), were detected within the survey area. The project specimens did not align closely with any previously detected species available for comparison.

Arachnida: Scorpionida – family Buthidae

Phylogenetic analysis confirmed the scorpion specimen collected belongs within the family Buthidae and aligns closely with a previously detected lineage belonging to be a known species complex (*Lychas 'annulatus complex'* H-SCB011). This lineage has previously been collected near De Grey, approximately 300 km west-northwest of the survey area specimen. This complex is suspected to have many undescribed species, some of which are considered SRE and others more widespread.

2.0 Introduction

2.1 Project Background

Biota Environmental Sciences engaged Helix Molecular Solutions (Helix) to undertake DNA extractions of terrestrial invertebrate fauna collected from a short-range endemic (SRE) survey of the Winu Borefields survey area. Specimens were to be sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COI). An additional inhouse primer set for the mitochondrial cytochrome b gene (CYB) was to be used for any mygalomorph spider specimens belonging to the family Idiopidae. Similarly, a multigene approach was requested for any scorpion specimens collected, which were to be sequenced using an additional 16S primer set. Analyses was undertaken to elucidate the taxonomic/phylogenetic relationships amongst the potential SRE invertebrate fauna.

A total of 11 invertebrate fauna specimens were collected from five sites from the survey area, which included 10 mygalomorph spiders (families Anamididae, Barychelidae and Idiopidae, based on field identifications) and one scorpion (family Buthidae). Specimens were submitted to Helix for DNA extraction and sequencing. Sequences were then analysed to determine the number of taxa present and their current known distributions or closest known locality outside the survey area based on comparisons with available genetic reference data.

This report provides a synopsis of the relationships between the successfully sequenced specimens and reference specimens available, including the number of putative species based on the phylogenetic analysis.

3.0 Methods

The 11 specimens, comprising four families based on morphology (Anamidae, Barychelidae, Idiopidae and Buthidae), were collected from five sampling sites. The specimens were sequenced for variation at COI using primers LCOI and HCO2 (Folmer et al., 1994). Two Idiopidae specimens were also sequenced for variation at CYB using an additional inhouse primer set. The primers used for CYB were 'CYBJ10612_id_f1' and 'CYB_Id_r1' from Rix et al. (2017a). The single buthid scorpion was also sequenced for variation of the mitochondrial LSU (large ribosomal subunit) 16S rRNA using an additional inhouse primer set: 'paraln_for' (Finston et al., 2011) and 'pmain16srev' (Helix, unpublished).

Sequences were edited using Geneious version 6.1.8 (<http://www.geneious.com>) performed within MEGA version 5.05 (Tamura et al., 2011) using the build-in alignment tool using CLUSTAL W (Thompson et al., 1994) default parameters. DNA nucleotide sequences were translated into protein sequences to ensure that the amplified sequences corresponded to the target mtDNA. The translated protein sequences were then checked for the presence of stop codons, to ensure that pseudogenes had not been amplified. Pseudogenes have a DNA sequence that is similar to the functional gene (e.g. COI) however, they do not code for a functioning protein despite the shared ancestry with the functional gene. The presence of pseudogenes can complicate molecular analyses, producing misleading results.

DNA sequences were translated into proteins with ExPASy using the invertebrate genetic code. All sequences analysed were of high quality with no evidence of heterogeneous peaks. All resulting sequences were 'BLAST'ed (Basic Local Alignment Search Tool) with the NCBI (National Centre for Biotechnology Information). The program compares DNA nucleotide sequences with a library of sequences and identifies sequences within the database that resemble the query sequences above a certain threshold. Genetic distance between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotides different between sequences). Un-corrected p-distances do not account for mutational saturation, which results from back mutations, and therefore provide a conservative estimate of genetic distance. To account for polymorphism within lineages, the net genetic diversity of Nei (1987) was calculated to give a 'corrected' distance between lineages.

For phylogenetic analysis, likelihood ratio tests using the Bayesian Information Criterion were calculated in MEGA 11 (Tamura et al., 2021) to determine the best-fit model of evolution. The phylogenetic analyses were conducted in Geneious Prime version 2024.0.5 (<https://www.geneious.com>) using the best-fit model of evolution calculated for each family (Table 3.1). Maximum likelihood (ML) analyses with 100 rapid bootstrap replicates were performed in RAxML (Randomised Accelerated Maximum Likelihood) version 8.2.11 (Stamatakis, 2014), using default settings.

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups between 3 to 5% sequence divergence. This cut-off was selected based on meta-reviews of bar-coding data, which indicate that intra-specific (within species) variation rarely exceeds 3% (Herbert et al., 2003b). Species were determined based on taxonomic group, molecular and morphological data available and previously published literature for each taxonomic group. For mygalomorph spiders, determining a cut-off value is problematic, particularly for the genus *Aname*. Castalanelli et al (2014) showed that 92% of the morphological species of Mygalomorphae were congruent with molecular species boundary based on 9.5% inter-specific (between species) pairwise divergence. One exception was the *Aname mellosa* species

complex, which showed 16.7% intra-specific diversity based on morphological identifications. However, COI data from that study determined 10 distinct genetic clades in the Pilbara and northern Gascoyne, showing distinct geographical clustering (Castalanelli et al., 2014), with 5 - 9% inter-clade genetic diversity. Rix et al. (2017b) found the mean intra-specific divergence ranged from 0% - 4.2% and mean inter-specific divergence ranged from 10.6% - 16.3% for a range of species belonging to the family Idiopidae. Based on these results, we have used a preliminary COI threshold of 9.5% divergence between lineages to assign putative species status. With additional morphological data and phylogenetic research this threshold may be modified where required. Helix species names have been updated for the current report to reflect our most current data and follow current Helix nomenclature (with nominal species names using the prefix 'H-').

Table 3.1: Best-fit model of evolution for each of the taxonomic groups and families analysed.

Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; G: Gamma; I: Invariant sites.

Analysis Group	Family/ Genus	Best Model	Gamma Value
Mygalomorphae	Anamidae	GTR + G + I	0.62
Mygalomorphae	Anamidae (<i>Kwonkan</i>)	GTR + G + I	0.69
Mygalomorphae	Halonoproctidae	GTR + G + I	0.85
Mygalomorphae	Idiopidae (COI)	GTR + G + I	0.60
Mygalomorphae	Idiopidae (CYB)	GTR + G + I	0.76
Scorpionida	Buthidae (COI)	GTR + G + I	0.88
Scorpionida	Buthidae (16S)	GTR + G + I	0.63

4.0 Results

Of the 11 specimens analysed, 10 were successfully sequenced for COI with two of the mygalomorph spider specimens from the family Idiopidae also sequenced for CYB and one buthid scorpion additionally sequenced for 16S (Table 4.1). Molecular family assignment matched the field morphological family identification for nine of the 10 specimens, with sequencing resulting in one reassignment. One specimen (TP08) was originally identified as belonging to the family Idiopidae but was reassigned following preliminary phylogenetic analysis as belonging to the family Halonoproctidae. The Barychelidae specimen failed to produce a high-quality sequence and was removed from further analysis.

Tables of genetic p-distance and associated standard errors between survey area specimens are provided in Appendix 1 (Table A1. 1 - Table A1. 3). Tables of genetic p-distances and associated standard errors of reference specimens showing less than 15 to 20% sequence divergence from survey area specimens are provided in Appendix 2 (Table A2. 1 -Table A2. 7).

Table 4.1: Invertebrate specimens used in the present study (n=11), and the genetic species to which they were assigned. Molecular lineages in bold text represent a newly detected lineage or species.

Specimen ID	Helix ID	Site	Latitude	Longitude	Taxonomic Group	Molecular Family ID	Molecular Genus ID	Molecular Species ID	Lineage
M20240301.WIB02SRE_MG-01	TP01	WIB02SRE	20°04'23.76"S	121°07'42.99"E	Mygalomorphae	Anamidae	<i>Aname</i>	H-N205	NTK
M20240301.WIB03SRE_MG-04	TP03	WIB03SRE	20°07'34.47"S	121°07'47.83"E	Mygalomorphae	Anamidae	<i>Aname</i>	H-N206	NTL
M20240301.WIB03SRE_MG-02	TP04	WIB03SRE	20°07'44.21"S	121°07'48.68"E	Mygalomorphae	Anamidae	<i>Aname</i>	H-N206	NTL
M20240301.WIB03SRE_MG-05	TP06	WIB03SRE	20°07'36.72"S	121°07'50.09"E	Mygalomorphae	Anamidae	<i>Aname</i>	H-N206	NTL
M20240301.WIB03SRE_MG-03	TP02	WIB03SRE	20°07'37.76"S	121°07'39.69"E	Mygalomorphae	Anamidae	<i>Kwonkan</i>	H-N197	NTM
M20240301.WIB03SRE_MG-01	TP05	WIB03SRE	20°07'44.20"S	121°07'48.61"E	Mygalomorphae	Anamidae	<i>Kwonkan</i>	H-N197	NTM
M20240513.WIB11SRE_MG-02	TP10	WIB11SRE	20°51'41.12"S	121°53'09.78"E	Mygalomorphae	Barychelidae	No data	No data	No data
M20240513.WIB12SRE_MG-02	TP08	WIB12SRE	20°51'56.57"S	121°53'14.80"E	Mygalomorphae	Halonoproctidae	<i>Conothele</i>	H-C29	CAV
M20240513.WIB12SRE_MG-01	TP07	WIB12SRE	20°51'56.83"S	121°53'16.09"E	Mygalomorphae	Idiopidae	<i>Idiosoma</i>	H-I90	IEA
M20240513.WIB11SRE_MG-01	TP09	WIB11SRE	20°51'40.83"S	121°53'09.40"E	Mygalomorphae	Idiopidae	<i>Idiosoma</i>	H-I91	IEB
S20240511.WIB07SRE_MG-01	TP11	WIB07SRE	20°52'55.32"S	121°51'54.28"E	Scorpionida	Buthid	<i>Lychas</i>	<i>Lychas annulatus</i>	SCB011

4.1 Mygalomorphae

The infraorder of Arachnida, Mygalomorphae, includes trapdoor spiders and their kin, which are frequently identified as SREs (e.g., Harvey et al., 2011; Castalanelli et al., 2014). This ancient group has a worldwide distribution that includes tarantulas, trapdoor spiders and funnel-web spiders (Opatova et al., 2020). Identification of species has traditionally been performed using morphological techniques, however, only males can be used in identification, as both females and juveniles lack the diagnostic characters used to delineate morphospecies and furthermore there is a large backlog of undescribed taxa.

Mygalomorph spider systematics has received a great deal of attention over the last decade as integrative molecular approaches have revolutionised our understanding of speciation, classification, and biogeography in these iconic arachnids (Rix et al., 2018). The morphological conservatism of the Mygalomorphae has been highlighted in these developments, which is often seemingly at odds with the very high levels of mitochondrial divergence observed in most taxa (Rix et al., 2018). Multi-locus approaches have revealed higher levels of diversity than anticipated (Rix et al., 2018). DNA barcoding with the use of COI has become a rapid, objective method aiding mygalomorph species identifications and their distributions and is recognised as providing important information that regulatory authorities can use to assess the environmental impacts of large-scale developments (Rix et al., 2008; Castalanelli et al., 2014). Extensive molecular work has been conducted on the trapdoor spider fauna of Western Australia (Helix, 2009a and b; 2010; 2011 a - l; 2012a – i; 2013a and b; 2014a – d; 2015a – e; 2018, 2019, 2020, 2021, 2022, 2023a-b, and 2024). The resulting dataset provides a molecular framework that can be used to provide regional context for localised sampling.

Ten Mygalomorphae specimens were collected from the survey area (Table 4.1). Nine of these specimens were successfully sequenced for COI (Table 4.1), with two of the Idiopidae specimens also successfully sequenced for CYB gene. One specimen (TP09) failed to sequence. Phylogenetic analysis confirmed a total of six species belonging to three families: Anamidae (n=3 species), Halonoproctidae (n=1 species), and Idiopidae (n=2 species).

4.1.1 Family Anamidae

The family Anamidae (previously Nemesiidae) is one of the most diverse and speciose mygalomorph families in Australia (Castalanelli et al., 2014; 2017; 2020, Harvey et al., 2020, Rix et al., 2021). It is considered the dominant trapdoor spider family in Australia (Castalanelli et al., 2020) and currently includes ten genera (*Aname*, L. Koch, 1873, *Chenistonia* Hogg, 1901, *Hesperonatalius*, Castalanelli et al., 2017, *Kwonkan* (including *Yilgarnia* and *Aname turrigera*), Main, 1983, *Namea*, Raven, 1984, *Proshermacha*, Simon, 1908, *Swolnpes*, Main and Framenau, 2009, *Teyl*, Main 1975, *Teyloides*, Main 1985 and *Troglodiplura* Main 1985). The most speciose of these genera, *Aname*, is found across most of Australia and is currently represented by 53 described species (World Spider Catalogue 2024).

Reference Specimens and Outgroups

Six specimens (TP01 – TP06), collected from two sites within the survey area (WIBO2SRE and WIBO3SRE), were assigned to the family Anamidae (Table 4.1). Survey area specimen sequences were analysed along with 885 reference specimens from both the Helix database (n=385) and GenBank (n=498). Preliminary analyses indicated that four of the specimens belonged within the genus *Aname* and two specimens belonged within the genus *Kwonkan*. Individual analyses were then undertaken with respect to each genus and a reduced dataset was used to simplify the phylogenetic tree for this report (Figure 4.1, Figure 4.2). However, full datasets were examined for relationships to reference specimens. All trees were rooted using two outgroups, *Centuroides vittatus* (GenBank #EU404114) and *Mesobuthus martensii* (GenBank #JF00146).

Phylogenetic Analyses

A 687 base-pair (bp) fragment of COI was isolated for each specimen from the survey area, resulting in 20 unique haplotypes. The six specimens were spread amongst three lineages (based on the >5% sequence divergence criterion) and three species (based on a 9.5% sequence divergence criterion), all of which were confirmed to sit within the family Anamidae (Table 4.2). Two of the species (n=4) aligned with reference specimens of *Aname* (Figure 4.1) and one of the species (n=2) aligned with reference specimens of *Kwonkan* (Figure 4.2).

Table 4.2: Summary of Anamidae species detected, showing number of specimens collected in each species and lineage, number of unique haplotypes sequenced, levels of Intra-specific (within species) pairwise genetic divergence (%) between project specimens and reference specimens, and inter-specific pairwise genetic divergence (between project specimens and next closest reference specimens). Newly detected lineages and species shown in bold.

Species	Lineage (>5%)	No. specimens	No. haplotypes	Intra-specific divergence (%) - project specimens	Intra-specific divergence (%) – Ref. specimens	Inter-specific divergence (%)
<i>Aname</i> sp. H-N205	NTK	1	1	N/A	N/A	11.7 (<i>A. sp.</i> MYG590)
<i>Aname</i> sp. H-N206	NTL	3	2	0.0 – 0.15 (TP03/04/06)	N/A	13.5- 15 (<i>A. watsoni</i>)
<i>Kwonkan</i> sp. H-N197	NTM	2	1	0.0 (TP02/05)	6.0 – 6.4 (H-N197)	11.6 (<i>K. sp.</i> H-N191)

Both species of *Aname* have not been previously detected outside the survey area and are considered to represent new species (Table 4.2). Relationships between survey area specimens and reference specimens currently available were poorly resolved within the phylogenetic tree, indicating no clear affiliation with previously detected lineages (Figure 4.1).

Analysis of the *Kwonkan* dataset showed that the two specimens from the survey area represent a new lineage of a previously recorded species, *Kwonkan* sp. H-N197. Specimens TP02 and TP05 formed a well-supported clade with representative specimens of *K. sp.* H-N197 (prefix 'SV'; Figure 4.2).

Differentiation within and between lineages/species

Phylogenetic analyses of the *Aname* group suggest that two species are present in the survey area. Amongst the four specimens of *Aname* collected from the survey area there was 0.0 – 13.7% molecular sequence divergence (Table A1. 1).

Aname sp. H-N205 is represented by a single specimen (TP01) and did not closely align with any previously detected lineage (Figure 4.1). The next closest reference specimens were *Aname* sp. MYG590 (GenBank #MW518637.1 WAMT101551) and *Aname grothi* (Helix #SV03/07/10 MYG373/H-N7) with inter-specific pairwise genetic divergences of 11.7% and 12.2% respectively (Table 4.2, Table A2. 1).

Aname sp. H-N206 is represented by three specimens (TP03, TP04 and TP06) and did not align closely with any previously detected lineage (Table 4.2). The next closest reference specimen was *Aname watsoni* (Helix# SY15) with an inter-specific pairwise genetic divergence of 13.5% (Table 4.2, Table A2. 1).

Phylogenetic analysis of the *Kwonkan* dataset showed that the two specimens from the survey area belong to one species of *Kwonkan* which has been previously recorded (Table 4.2, Figure 4.2). One new lineage of a previous detected species, *Kwonkan* sp. H-N197, was detected from the survey area specimens. It differed from the reference specimens of *K. sp.* H-N197 (Helix #s SV41, SV47, SV25) by 6.0 – 6.4% pairwise genetic divergence (Table 4.2, Table A2. 2). The next closest reference specimen was *Kwonkan* sp. H-N191 (Helix # SS09) with 11.6% inter-specific pairwise genetic divergence (Table 4.2, Table A2. 2).

Conclusions

Three species of Anamidae have been detected in the survey area, corresponding to two *Aname* species and one *Kwonkan* species. Of the three species detected during the survey, two were new putative species (*Aname* sp. H-N205 and *A. sp.* H-N206) as they differed from the nearest reference specimens by >9.5%. The remaining species represents a new lineage of *Kwonkan* sp. H-N197, which has previously been collected approximately 245 km west of the survey area.



Aname sp. H-N205

Aname sp. H-N206

Figure 4.1:

Maximum Likelihood (ML) analysis of *Aname* COI mtDNA sequences, showing the placement of the survey area specimens ('TP' prefix) and two species designations (coloured in blue and orange), within a reduced taxonomic framework of the family Anamidae. ML tree is for illustrative purposes only with a complete ML tree available on request. Numbers on nodes indicate nodal support by means of ML bootstrap values. Scale indicates inferred evolutionary distance (substitutions/site).

Helix

4.1.2 Family Halonoproctidae

The family Halonoproctidae was previously a subfamily of the Ctenizidae until it was recently separated (Godwin et al., 2018), and currently comprises six genera and more than 80 species. Godwin et al. (2018) found two phylogenetically well-supported subclades within the Halonoproctidae that were morphologically distinguishable, one now the newly named subfamily Halonoproctinae, the other was circumscribed Ummidiinae. The Halonoproctidae family is distributed on all the continents, with the exception of Antarctica (Godwin et al., 2018).

The Australian Halonoproctidae are likely to belong to the genus *Conothele* (Thorell, 1878), which are also found in Asia, New Guinea and other island groups (Godwin et al., 2018). Currently there are 36 described species of *Conothele*, but only two species are currently described from Australia (World Spider Catalog 2024). Within Australia, *Conothele* occur in the monsoonal tropics, arid and semiarid zones and are generally fossorial, living in burrows plugged with tightly sealed trapdoor lids. Recent phylogenetic studies have indicated that the genus is highly diverse in Western Australia with numerous undocumented and undescribed short range endemic lineages (Huey et al., 2019, Harvey 2002, Castalanelli et al., 2014).

Reference Specimens and Outgroups

A single specimen collected initially identified as belonging to the family Idiopidae was reassigned to Halonoproctidae (Table 4.3). This Halonoproctidae COI sequence was analysed along with 180 reference specimens from both the Helix database (n=35) and GenBank (n=145). The specimen was identified as belonging to the genus *Conothele*. Phylogenetic trees were rooted using two outgroups, *Centuroides vittatus* (GenBank #EU404114) and *Mesobuthus martensii* (GenBank #JF00146).

Phylogenetic Analyses

A 737 base-pair fragment of COI was isolated for this specimen, resulting in a single unique haplotype. The haplotype falls within the family Halonoproctidae and the genus *Conothele*. According to the molecular sequence data currently available for comparison, the specimen aligns with reference specimens belonging to a recently detected species *Conothele* sp. H-C29, forming a well-supported clade.

Table 4.3: Summary of Halonoproctidae detected, showing number of specimens collected in each species and lineage, number of unique haplotypes sequenced, levels of Intra-specific (within species) pairwise genetic divergence (%) between project specimens and reference specimens, and inter-specific pairwise genetic divergence (between project specimens and next closest reference specimens). Newly detected lineages and species shown in bold.

Species	Lineage (>5%)	No. specimens	No. haplotypes	Intra-specific divergence (%) - project specimens	Intra-specific divergence (%) – Ref. specimens	Inter-specific divergence (%)
<i>Conothele</i> sp. H-C29	CAV	1	1	N/A	7.0 – 8.0 (H-C29)	9.1 (C. sp. H-C27)

Differentiation within and between species/lineages

The survey area specimen (TP08) represents a new lineage (CAV) of a previously detected species *Conothele* sp. H-C29 and differs from these specimens by 7.0 - 8.0% pairwise genetic divergence (Table 4.3). The next closest reference specimen was *Conothele* sp. H-C27 (Helix # OY10 H-C27 T148197 – Helix # OY14 H-C27 T148201), showing 9.1% and 10.5% pairwise genetic divergence respectively (Table A2. 3).

Conclusions

One new lineage of a previously detected species (*C. sp. H-C29*) was detected during the survey. The new specimen (TP08) was collected from approximately 290 km east of the five reference specimens (Helix #SV56, SV57, SV58, SV60 and SV61; Helix 2023b). The next closest reference species to *C. sp. H-C29* was *C. sp. H-C27*, which is known from southwest of Onslow, almost 500 km from the survey area specimen (Helix 2023b).

Helix

4.1.3 Family Idiopidae

The spiny trapdoor spiders (Idiopidae) encompass the Australasian endemic subfamily Arbanitinae (Rix et al., 2017a-c). The family has a distribution consistent with the former Gondwanan land masses, and they are largely undescribed at the species level and have a confusing taxonomic history at the generic level (Rix et al., 2017a). Taxonomic revisions using molecular data within Idiopidae have shown that a multi-gene approach is necessary for some species (Wilson et al., 2019). Previous discussions with Dr Mike Rix of the Queensland Museum, who authored the *Gaius* revision (Rix et al., 2018) using this approach, led to the decision to standardise sequencing for Idiopidae specimens by including both COI and CYB gene regions.

Reference Specimens and Outgroups

Three specimens from two sites within the survey area were initially identified as belonging to the family Idiopidae (Table 4.1). One specimen (TP08) was reassigned to Halonoproctidae following preliminary molecular analysis. The resulting two Idiopidae samples (TP07 and TP09) were successfully sequenced for both COI and CYB (Table 4.1). The COI sequenced specimens were analysed along with a total of 261 reference specimens sequenced for COI from both the Helix database (n=161) and GenBank (n=100), including outgroups *Centruroides vittatus* (GenBank #EU404114) and *Mesobuthus martensii* (GenBank #JF700146) (Figure 4.5). The representative haplotypes of the CYB idiopid specimens were analysed along with 221 reference specimens from both the Helix database (n=95) and GenBank (n=126), which included outgroups *Mesobuthus cyprius* (GenBank #DQ323712) and *Mesobuthus gibbosus* (GenBank #DQ323730) (Figure 4.6).

Phylogenetic Analyses

A 734 bp fragment of CYB was isolated for specimens TP07 and TP09. A standard 687 bp fragment of COI was also isolated for specimen TP07 but a smaller 441 bp fragment of COI was isolated for TP09. The resulting haplotypes were confirmed to sit within the Idiopidae (Table 4.4, Table 4.5). Phylogenetic analysis of the COI and CYB data detected two lineages, representing two putative species belonging to the genus *Idiosoma* (Figure 4.5, Figure 4.6). Two new species, *Idiosoma* sp. H-I90 and *I.* sp. H-I91, were detected. The CYB phylogenetic analysis showed that specimen TP09 (*I.* sp. H-I91) formed a well-supported clade with reference specimens of *Idiosoma* sp. H-I89, H-I82, H-I87 and H-I85 (Figure 4.6). Specimen TP07 did not align closely with reference specimens available for either analysis (Figure 4.5, Figure 4.6).

Table 4.4: Summary of the Idiopidae species detected in the survey area, showing number of specimens collected, number of unique haplotypes sequenced for COI, levels of intra-specific (within species) pairwise genetic divergence (%) between project specimen and reference specimens, and inter-specific pairwise genetic divergence (between project specimen and next closest reference specimens). Newly detected lineages and species shown in bold.

Species	Lineage (>5%)	No. specimens	No. haplotypes	Intra-specific divergence (%) - project specimens	Intra-specific divergence (%) – Ref. specimens	Inter-specific divergence (%)
<i>Idiosoma</i> sp. H-I90	IEA	1	1	N/A	N/A	12.7 (<i>I. sp.</i> MYG256/H-I65)
<i>Idiosoma</i> sp. H-I91	IEB	1	1	N/A	N/A	11.4 (<i>I. sp.</i> H-I57)

Table 4.5: Summary of the Idiopidae species detected in the survey area, showing number of specimens collected, number of unique haplotypes sequenced for CYB, levels of intra-specific (within species) pairwise genetic divergence (%) between project specimen and reference specimens, and inter-specific pairwise genetic divergence (between project specimen and next closest reference specimens). Newly detected lineages and species shown in bold.

Species	Lineage (>5%)	No. specimens	No. haplotypes	Intra-specific divergence (%) - project specimens	Intra-specific divergence (%) – Ref. specimens	Inter-specific divergence (%)
<i>Idiosoma</i> sp. H-I90	IEA	1	1	N/A	N/A	17.9 (<i>I. sp.</i> WAM T110336)
<i>Idiosoma</i> sp. H-I91	IEB	1	1	N/A	N/A	16 (<i>I. sp.</i> WAM T101994)

Differentiation within and between lineages

Analysis of the COI and CYB data detected two unique lineages showing 15.6% pairwise sequence divergence for COI (Table A1. 2) and 21.2% pairwise sequence divergence for CYB (Table A1. 3).

The new species *Idiosoma* sp. H-I90 (specimen TP07) and *I. sp.* H-I91 (specimen TP09) are each represented by a single specimen and did not closely align with any previously detected lineage (Figure 4.5, Figure 4.6). The closest reference specimen to *I. sp.* H-I90 was *I. sp.* MYG254/H-I65 (Helix #s SB06, SB13, SB19, SB17 and GenBank #KJ745099 *I. sp.* MYG256 T123106) showing between 12.7 and 13.8% pairwise genetic divergence for COI (Table 4.4, Table A2. 4).

Phylogenetic analyses using CYB molecular data showed that *I. sp.* WAM T110336 (GenBank #KY295396) was the next closest reference specimen, with 17.9% interspecific pairwise genetic divergence. For comparison, COI analysis of *I. sp.* WAM T110336 (GenBank #KY295274) showed a pairwise genetic divergence from project specimen TP07 of 15.4% (Table A2. 4), whereas CYB phylogenetic analysis of *I. MYG265/H-I65* reference sequences showed 19 – 19.9% pairwise genetic divergence (Table A2. 5).

The closest reference specimen to *I. sp.* H-I91 was *Idiosoma* sp. MYG300/H-I57 (Helix #s BV011 H-I57 and GenBank #KJ744981 *Idiosoma* sp. MYG300 T122206) showing between 11.4 and 11.7% pairwise genetic divergence for COI (Table 4.4). The closest reference specimen to the CYB sequence was *Idiosoma* sp. WAM T101994 (GenBank #KY295443), with a pairwise genetic divergence of 16% (Table 4.5, Table A2. 5). The equivalent COI sequence for *Idiosoma* sp. WAM T101994 (GenBank #KY295322) showed 15% pairwise genetic divergence (Table A2. 4).

Conclusions

Two new species of Idiopidae, *Idiosoma* sp. H-I90 and *I.* sp. H-I91, have been detected from the survey area. The new species differ from the nearest reference specimens by more than 11% (COI; Table 4.4) and 16% (CYB; Table 4.5). The closest reference specimens to *Idiosoma* sp. H-I90 were collected over 900 km south southwest of the survey area. The closest reference specimens to *I.* sp. H-I91 were collected approximately 360 km southwest of the survey area.

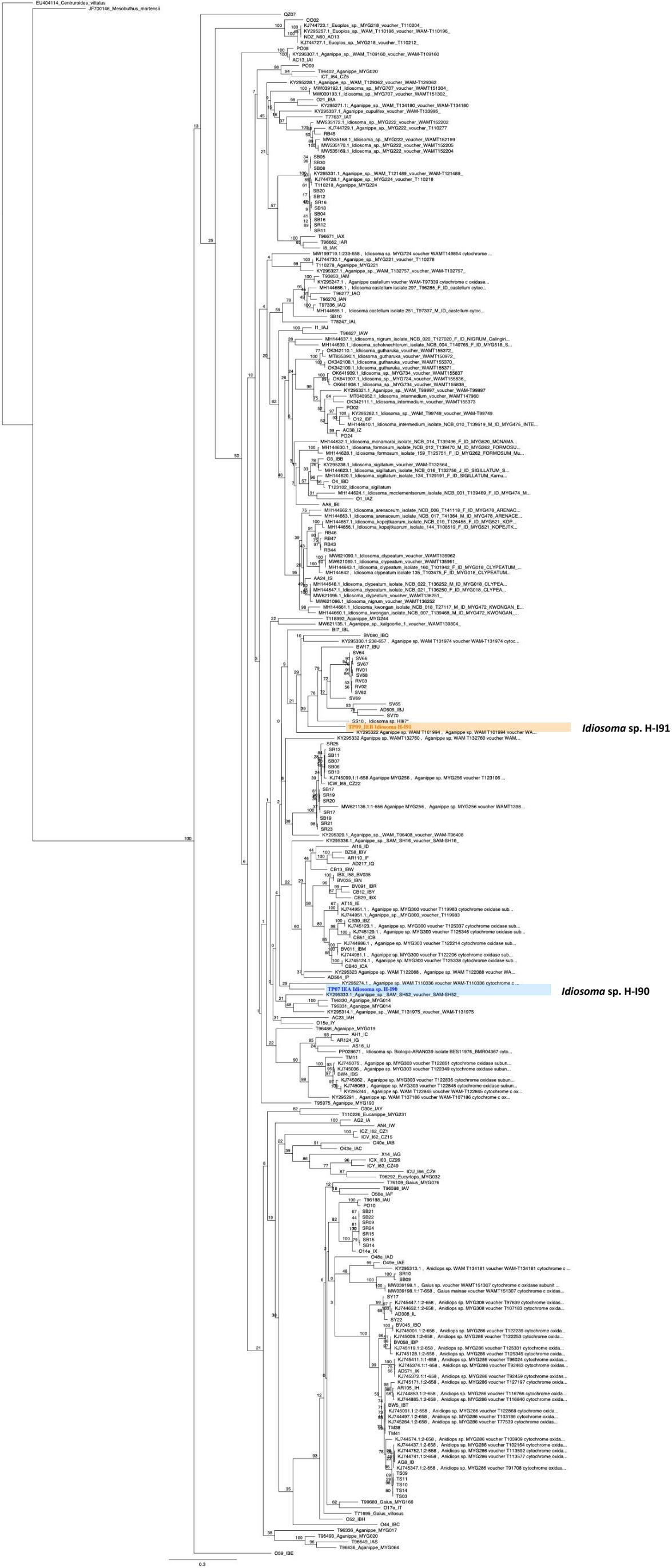


Figure 4.4: Maximum Likelihood analysis of *Idiosoma* COI mtDNA sequences, showing the placement of the survey area specimens ('TP' prefix) and species designation (coloured in blue and orange), within the taxonomic framework of the family Idiopidae including 261 reference specimens. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Scale indicates inferred evolutionary distance (substitutions/site).



Figure 4.5: Maximum Likelihood analysis of *Idiosoma* CYB mtDNA sequences, showing the placement of the survey area specimens (‘TP’ prefix) and species designation (coloured in blue and orange), within the taxonomic framework of the family Idiopidae including 221 reference specimens. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Scale indicates inferred evolutionary distance (substitutions/site)

4.2 Scorpionida

4.2.1 Family Buthidae

The Buthidae family is the largest group of scorpions, currently comprising 1,255 species across 94 extant genera (Rein, 2024). They are found worldwide, except Antarctica and New Zealand, and inhabit tropical, subtropical and temperate regions. Despite being one of the oldest and most diverse scorpion families, their phylogenetic relationships remain poorly understood (Stundalova et al., 2022). There are very few molecular investigations of phylogenetic relationships undertaken for Buthidae (Gantenbein et al., 2000; 2003; Fet et al., 2003; Gantenbein and Largiadèr, 2003; Mirshamsi et al., 2010; Sousa et al., 2010, 2011; Suranse et al., 2017). These studies indicate that traditional morpho-taxonomy is limited in defining species boundaries, with many recognised species potentially being species complexes comprising undescribed taxa. The morphological variability within and similarly between taxa has led to taxonomic confusion, highlighting the need for molecular data to accurately delineate species (Yamashita and Rhoads, 2013). A combined multigene approach is recommended for better clarity, and some genera require further taxonomic revision (Stundalova et al., 2022).

The Buthidae genus *Lychas* is a diverse genus of small scorpions, with 33 currently described species (Rein, 2024). Within Australia there are many more known but undescribed species, particularly from the Pilbara region.

One scorpion specimen identified as belonging to the family Buthidae was collected within the survey area and subsequently sequenced for COI and 16S (Table 4.1).

Reference Specimens and Outgroups

The COI sequence of specimen TP11 was analysed along with an initial 145 reference specimens from both the Helix database (n=29) and GenBank (n=116). The outgroup, *Pandinus dictator* (GenBank #AY156581), was used to root the COI phylogenetic tree (Figure 4.7). The 16S sequence was analysed along with 131 reference sequences from GenBank, with *Pseudochactas ovchinnikovi* (Pseudochactidae) as an outgroup (GenBank #AY226167). There are very few sequences available of specimens occurring within Australia as reference.

Phylogenetic Analyses

A 687 bp fragment of COI and a 344 bp fragment of 16S was isolated specimen TP11. According to the molecular sequence data currently available for comparison, the specimen was confirmed to sit within the family Buthidae (Figure 4.7, Table 4.6).

The specimen TP11 aligned closely with one COI reference sequence available but did not align with any 16S reference sequences available. The survey area specimen represents a known lineage of a species complex *Lychas* '*annulatus* complex' (SCB011). Consultation with Erich Volschenk of Alacran Environmental Science, confirms this placement of the specimen within his more extensive sequence database for Scorpionida.

Table 4.6: Summary of the Buthidae species detected in the survey area, showing number of specimens collected, number of unique haplotypes sequenced for COI and 16S, levels of intra-specific (within species) pairwise genetic divergence (%) between project specimen and reference specimens, and inter-specific pairwise genetic divergence (between project specimen and next closest reference specimens). Newly detected lineages and species shown in bold.

Species	Lineage (>5%)	No. specimens	No. haplotypes	Intra-specific divergence (%) - project specimens	Intra-specific divergence (%) – Ref. specimens	Inter-specific divergence (%)
<i>Lychas</i> ‘annulatus complex’ – COI	SCB011	1	1	N/A	4.2 (Helix #SV73)	9.6 (<i>L. sp.</i> Biologic-SCOR012)
<i>Lychas</i> ‘annulatus complex’ – 16S		1	1	N/A	N/A	17 (<i>Isometrus lithophilis</i>)

Differentiation within and between lineages

Phylogenetic analysis of the Buthidae COI dataset showed that specimen TP11 belong to a lineage of *Lychas* that has been previously recorded (Table 4.6, Figure 4.7). Specimen TP11 aligned with a reference specimen of *Lychas* ‘annulatus complex’ (Helix #SV73) with an intra-specific pairwise genetic divergence of 4.2% (Table 4.6). The next closest reference specimen was *Lychas* sp. Biologic- SCOR012 (GenBank #PP028575), with an inter-specific pairwise sequence divergence of 9.6% (Table 4.6, Table A2. 6).

Phylogenetic analyses using 16S molecular data showed that *Isometrus lithophilis* (GenBank #OR802156) and *Lychas mucronatus* (GenBank #AF370855) were the next closest reference specimens, with 17.0% and 17.5% interspecific pairwise genetic divergences respectively (Table A2. 7). For comparison, COI analysis of *Lychas mucronatus* (GenBank #JN018153 and #NC072215) showed pairwise genetic divergences from project specimen TP11 of 13.8% - 13.9% (Table A2. 6). The reference specimens *Lychas* ‘annulatus complex’ (Helix #SV73) and *Lychas* sp. Biologic- SCOR012 did not have corresponding 16S sequences and was hence unavailable for comparison within the 16S dataset.

Survey area specimen TP11 represents a previously detected *Lychas* taxon (*Lychas* ‘annulatus complex’) according to the molecular genetic data currently available for comparison.

Conclusions

One previously detected buthid scorpion taxon (*Lychas* ‘annulatus complex’) was detected (Table 4.6, Figure 4.7, Figure 4.8). The closest reference specimen of this species was detected approximately 300 km west southwest of the survey area. *Lychas* sp. Biologic-SCOR012 was detected approximately 340 km southwest of the survey area. Both *Isometrus lithophilis* and *Lychas mucronatus* do not occur in Australia. *Lychas mucronatus* is a Chinese swimming scorpion which is widespread throughout Southeast Asia. Very few Australian Buthidae 16S sequences are available on GenBank despite a multigene approach, particularly the use of the 16S gene region, being recommended to resolve phylogenetic relationships within this family.

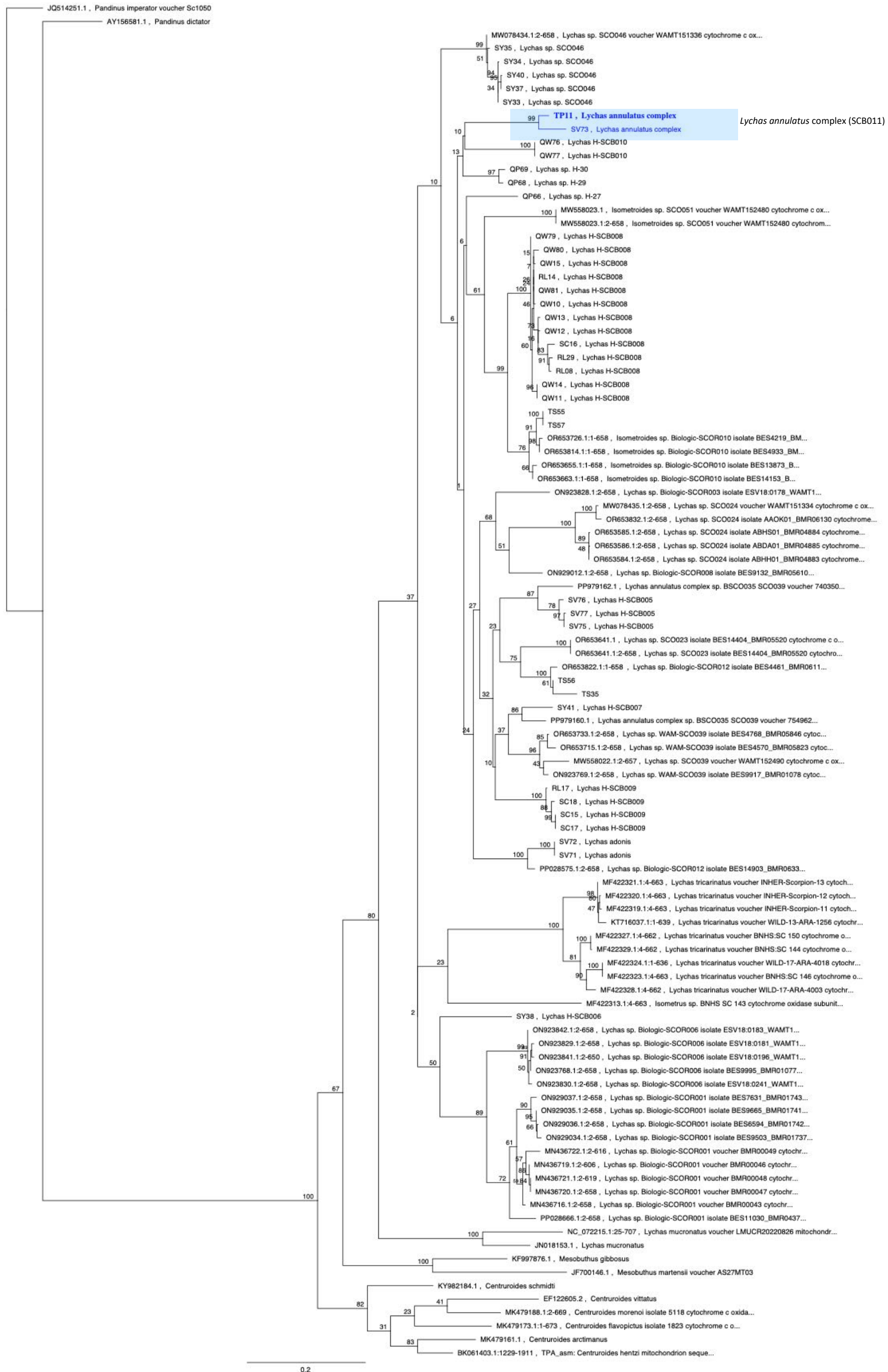


Figure 4.6: Maximum Likelihood analysis of *Lychas* COI mtDNA sequences, showing the placement of the survey area specimen ('TP' prefix) and species designation (coloured in blue), within a reduced taxonomic framework of the family Buthidae (original analysis included 145 reference specimens). Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Scale indicates inferred evolutionary distance (substitutions/site).



Figure 4.7: Maximum Likelihood analysis of *Lychas* 16S mtDNA sequences, showing the placement of the survey area specimen ('TP' prefix) and species designation (coloured in blue), within the taxonomic framework of the family Buthidae including 131 reference specimens. Numbers on nodes indicate nodal support by means of maximum likelihood (ML) bootstrap values. Scale indicates inferred evolutionary distance (substitutions/site).

5.0 Discussion

COI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a) and the use of this gene can be extremely effective for DNA barcoding in taxa where clear differentiation exists between intra and interspecific levels of divergence (e.g. Hebert et al., 2004a; 2004b). In a comparison of COI sequences for over 13,000 pairs of taxa, Hebert et al., (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of these comparisons found that species pairs differed from one another by >8% sequence divergence.

Despite its merits in barcoding, a taxon-by-taxon approach, examining the amount of phylogenetic variation within and between taxa is the most widely accepted method of delineating species and their distributions, especially in areas where rapidly expanding development outpaces taxonomic treatment of unresolved taxa.

Of the 11 potential SRE specimens collected from the survey area, 10 were sequenced for COI, two of the mygalomorph spider specimens from the family Idiopidae also sequenced for CYB, and one buthid scorpion sequenced for 16S (Table 4.1).

In summary, we detected a total of seven putative species from four families, comprising:

Mygalomorphae: Anamidae n=3, Halonoproctidae n=1 and Idiopidae n=2; and

Scorpionidae: Buthidae n=1.

Of the seven species detected, two align with previously detected but undescribed widespread species, one aligned with a known lineage of a previously recorded species-complex, and four are newly detected putative species currently only known from the survey area.

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- Helix 2012h.** Report on the molecular systematics of Mygalomorphae from West Turner Extension. Unpublished report for Biota Environmental Sciences.
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Appendix 1 Genetic p-distances between Winu survey specimens

Table A1. 1: Genetic p-distance (below) and associated standard error (above- **blue text**) between the four *Aname* and two *Kwonkan* (Anamidae) COI specimens from this study ('TP' prefix).

		<i>Kwonkan</i>		<i>Aname</i>			
Molecular sp. ID		TP02	TP05	TP03	TP04	TP06	TP01
<i>Kwonkan</i>	H-N197	TP02	0.00000	0.01467	0.01467	0.01472	0.01414
		TP05	0.00000	0.01467	0.01467	0.01472	0.01414
<i>Aname</i>	H-N206	TP03	0.18049	0.18049	0.00000	0.00145	0.01311
		TP04	0.18049	0.18049	0.00000	0.00145	0.01311
		TP06	0.18195	0.18195	0.00146	0.00146	0.01305
	H-N205	TP01	0.16448	0.16448	0.13683	0.13683	0.13537

Table A1. 2: Genetic p-distance (below) and associated standard error (above- **blue text**) between the two COI sequenced *Idiosoma* (Idiopidae) specimens from this study ('TP' prefix).

		<i>Idiosoma</i>	
Molecular sp. ID		TP09	TP07
<i>Idiosoma</i>	H-I91	TP09	0.01730
	H-I90	TP07	0.15646

Table A1. 3: Genetic p-distance (below) and associated standard error (above- **blue text**) between the two CYB sequenced *Idiosoma* (Idiopidae) specimens from this study ('TP' prefix).

		<i>Idiosoma</i>	
Molecular sp. ID		TP09	TP07
<i>Idiosoma</i>	H-I91	TP09	0.01519
	H-I90	TP07	0.21241



Appendix 2 Genetic p-distances between Winu survey specimens and reference specimens

Table A2. 1: Genetic p-distance and the associated standard error from reference specimens showing less than 15% sequence divergence from the two *Aname* species TP01 (Molecular ID: *Aname* sp. H-N205) and TP03/04/06 (Molecular ID: *A. sp.* H-N206).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP03	TP04	0.0000	0.0000
TP03	TP06	0.0015	0.0015
TP06	TP03	0.0015	0.0015
TP06	TP04	0.0015	0.0015
TP01	MW518637.1 <i>Aname</i> sp. MYG590 isolate WAMT101551	0.1169	0.0157
TP01	SV07 NSS <i>Aname grothi</i> MYG373 (H-N7)	0.1218	0.0157
TP01	SV10 NSS <i>Aname grothi</i> MYG373 (H-N7)	0.1218	0.0157
TP01	SV03 NBT <i>Aname grothi</i> MYG373 (H-N7)	0.1266	0.0127
TP01	NBF N11 AD592	0.1289	0.0164
TP01	SV01 NBT <i>Aname grothi</i> MYG373 (H-N7)	0.1295	0.0128
TP01	MW518631.1 <i>Aname</i> sp. MYG647 isolate WAMT92169	0.1310	0.0165
TP01	SV11 NBT <i>Aname grothi</i> MYG373 (H-N7)	0.1310	0.0162
TP01	SV14 NBT <i>Aname grothi</i> MYG373 (H-N7)	0.1310	0.0162
TP01	KJ744911.1 <i>Aname</i> sp. MYG331 T118812	0.1337	0.0133
TP01	KJ744909.1 <i>Aname</i> sp. MYG331 T118805	0.1353	0.0133
TP01	KJ744914.1 <i>Aname</i> sp. MYG331 T118818	0.1353	0.0133
TP01	MW518618.1 <i>Aname</i> sp. MYG686 isolate SAMNN28448	0.1353	0.0133
TP01	SV30 NSV <i>Aname</i> H-N193	0.1354	0.0131
TP01	SV35 NSW <i>Aname</i> H-N194	0.1354	0.0131
TP01	SV36 NSW <i>Aname</i> H-N194	0.1354	0.0131
TP01	TP06	0.1354	0.0131
TP03	SY15 NTF <i>Aname watsoni</i>	0.1354	0.0131
TP03	SY16 NTF <i>Aname watsoni</i>	0.1354	0.0131
TP03	SY18 NTF <i>Aname watsoni</i>	0.1354	0.0131
TP03	SY24 NTF <i>Aname watsoni</i>	0.1354	0.0131
TP06	TP01	0.1354	0.0131
TP01	MN635075.1 <i>Aname grothi</i> voucher WAMT133820	0.1355	0.0134
TP01	MW518656.1 <i>Aname</i> sp. MYG276 isolate WAMT130451	0.1360	0.0167
TP01	MW518669.1 <i>Aname</i> sp. MYG590 isolate WAMT144388	0.1360	0.0167
TP01	NBT N7 AD748	0.1360	0.0167
TP01	NRG N7 NN15	0.1360	0.0167
TP01	QP44 H-N159	0.1360	0.0167
TP01	KJ744902.1 <i>Aname</i> sp. MYG331 T118791	0.1368	0.0134
TP01	TP03	0.1368	0.0131
TP01	TP04	0.1368	0.0131
TP03	SS06 <i>Aname</i> sp. H-N190	0.1368	0.0131
TP03	TP01	0.1368	0.0131
TP06	SY15 NTF <i>Aname watsoni</i>	0.1368	0.0131
TP06	SY16 NTF <i>Aname watsoni</i>	0.1368	0.0131
TP06	SY18 NTF <i>Aname watsoni</i>	0.1368	0.0131
TP06	SY24 NTF <i>Aname watsoni</i>	0.1368	0.0131
TP03	KJ744454.1 <i>Aname mellosa</i> voucher T102738	0.1370	0.0134
TP03	OY09 NRU H-N146	0.1373	0.0133
TP03	TS12	0.1383	0.0132
TP06	SS06 <i>Aname</i> sp. H-N190	0.1383	0.0132
TP01	KJ744901.1 <i>Aname</i> sp. MYG331 T118789	0.1383	0.0135
TP01	KJ744910.1 <i>Aname</i> sp. MYG331 T118811	0.1383	0.0135
TP01	KJ745407.1 <i>Aname</i> sp. MYG366 T96018	0.1383	0.0135
TP01	KJ744610.1 <i>Aname</i> sp. MYG371 T105216	0.1384	0.0169
TP01	NBR N14 AD746	0.1384	0.0169

Project specimen	Reference Specimen	P-Distance	Std. Err
TP01	NEH N112 BI22	0.1384	0.0169
TP01	NRF N7 NN11	0.1384	0.0169
TP01	MW518658.1 <i>Aname</i> sp. MYG285 isolate WAMT131132	0.1385	0.0135
TP03	KJ744456.1 <i>Aname mellosa</i> voucher T102740	0.1385	0.0135
TP06	KJ744454.1 <i>Aname mellosa</i> voucher T102738	0.1385	0.0135
TP01	QZ04	0.1388	0.0134
TP01	RL26	0.1388	0.0134
TP06	OY09 NRU H-N146	0.1388	0.0134
TP03	MN433239.1 <i>Aname mellosa</i> isolate OV29	0.1396	0.0134
TP01	SJ02 <i>Aname</i> H-N187	0.1397	0.0132
TP01	TM12	0.1397	0.0132
TP01	TM17	0.1397	0.0132
TP03	TM07	0.1397	0.0132
TP03	TM28	0.1397	0.0132
TP06	TS12	0.1397	0.0132
TP03	KJ745326.1 <i>Aname mellosa</i> voucher T88698	0.1398	0.0135
TP03	KJ745333.1 <i>Aname mellosa</i> voucher T88705	0.1398	0.0135
TP06	KJ744456.1 <i>Aname mellosa</i> voucher T102740	0.1400	0.0135
TP01	PO35 NAG H-N113	0.1403	0.0134
TP03	MN635068.1 <i>Aname watsoni</i> voucher WAMT104786	0.1407	0.0192
TP01	MG800157.1 <i>Aname</i> sp. MYG411 WAMT94952	0.1408	0.0170
TP01	NDW OO11 N57	0.1408	0.0170
TP01	NDW OY25 N57	0.1408	0.0170
TP01	NRJ N7 NN18	0.1408	0.0170
TP01	OO11 H-N57	0.1408	0.0170
TP01	QP58 H-N159	0.1408	0.0170
TP01	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1410	0.0149
TP03	MN433233.1 <i>Aname mellosa</i> isolate OV19	0.1411	0.0135
TP03	MN433238.1 <i>Aname mellosa</i> isolate OV25	0.1411	0.0135
TP03	MN433255.1 <i>Aname mellosa</i> isolate OV66	0.1411	0.0135
TP03	MN433257.1 <i>Aname mellosa</i> isolate OV71	0.1411	0.0135
TP06	MN433239.1 <i>Aname mellosa</i> isolate OV29	0.1411	0.0135
TP01	SV31	0.1412	0.0133
TP01	SY11 NTE <i>Aname</i> H-N203	0.1412	0.0133
TP01	TM04	0.1412	0.0133
TP01	TM08	0.1412	0.0133
TP01	TM10	0.1412	0.0133
TP01	TM16	0.1412	0.0133
TP01	TM27	0.1412	0.0133
TP03	TM08	0.1412	0.0133
TP03	TM10	0.1412	0.0133
TP06	TM07	0.1412	0.0133
TP06	TM28	0.1412	0.0133
TP01	KJ744648.1 <i>Aname</i> sp. MYG373 T107087	0.1413	0.0136
TP01	MW518632.1 <i>Aname</i> sp. MYG411 isolate WAMT94952	0.1413	0.0136
TP03	KJ745316.1 <i>Aname mellosa</i> voucher T88671	0.1413	0.0136
TP03	KJ745330.1 <i>Aname mellosa</i> voucher T88702	0.1413	0.0136
TP03	KJ745334.1 <i>Aname mellosa</i> voucher T88707	0.1413	0.0136
TP06	KJ745326.1 <i>Aname mellosa</i> voucher T88698	0.1413	0.0136
TP06	KJ745333.1 <i>Aname mellosa</i> voucher T88705	0.1413	0.0136
TP06	KJ745407.1 <i>Aname</i> sp. MYG366 T96018	0.1413	0.0136
TP01	MW518645.1 <i>Aname</i> sp. MYG223 isolate WAMT110282	0.1416	0.0136
TP03	KJ744451.1 <i>Aname mellosa</i> voucher T102735	0.1416	0.0136
TP01	MN635073.1 <i>Aname sinuata</i> voucher WAMT129020	0.1425	0.0176

Project specimen	Reference Specimen	P-Distance	Std. Err
TP01	MN635074.1 <i>Aname sinuata</i> voucher WAMT129021	0.1425	0.0176
TP03	MN433240.1 <i>Aname mellosa</i> isolate OV30	0.1426	0.0136
TP03	MN433243.1 <i>Aname mellosa</i> isolate OV38	0.1426	0.0136
TP03	MN433248.1 <i>Aname mellosa</i> isolate OV53	0.1426	0.0136
TP03	MN433253.1 <i>Aname mellosa</i> isolate OV63	0.1426	0.0136
TP03	MN433254.1 <i>Aname mellosa</i> isolate OV65	0.1426	0.0136
TP06	MN433233.1 <i>Aname mellosa</i> isolate OV19	0.1426	0.0136
TP06	MN433238.1 <i>Aname mellosa</i> isolate OV25	0.1426	0.0136
TP06	MN433255.1 <i>Aname mellosa</i> isolate OV66	0.1426	0.0136
TP06	MN433257.1 <i>Aname mellosa</i> isolate OV71	0.1426	0.0136
TP01	SV33	0.1426	0.0133
TP01	SY12 NTE <i>Aname</i> H-N203	0.1426	0.0133
TP01	TM02	0.1426	0.0133
TP01	TM03	0.1426	0.0133
TP01	TM14	0.1426	0.0133
TP01	TM24	0.1426	0.0133
TP03	SS07 <i>Aname</i> sp. H-N190	0.1426	0.0133
TP03	TM39	0.1426	0.0133
TP06	TM08	0.1426	0.0133
TP06	TM10	0.1426	0.0133
TP01	KJ745239.1 <i>Aname</i> sp. MYG177 T74755(2)	0.1429	0.0136
TP03	JQ772133.1 <i>Aname</i> sp. 4 MGR-2012 voucher WAM:T96140	0.1429	0.0138
TP03	KJ745327.1 <i>Aname mellosa</i> voucher T88699	0.1429	0.0136
TP03	KJ745339.1 <i>Aname mellosa</i> voucher T88713	0.1429	0.0136
TP03	KJ745407.1 <i>Aname</i> sp. MYG366 T96018	0.1429	0.0136
TP06	KJ745316.1 <i>Aname mellosa</i> voucher T88671	0.1429	0.0136
TP06	KJ745330.1 <i>Aname mellosa</i> voucher T88702	0.1429	0.0136
TP06	KJ745334.1 <i>Aname mellosa</i> voucher T88707	0.1429	0.0136
TP01	SB33	0.1431	0.0134
TP01	KJ744611.1 <i>Aname mellosa</i> T10585	0.1431	0.0137
TP06	KJ744451.1 <i>Aname mellosa</i> voucher T102735	0.1431	0.0137
TP01	KJ745242.1 <i>Aname</i> sp. MYG177 T76820	0.1432	0.0171
TP01	NGI N131 CZ41	0.1432	0.0171
TP01	NRH N7 NN16	0.1432	0.0171
TP01	NRI N7 NN17	0.1432	0.0171
TP01	NRK N7 NN20	0.1432	0.0171
TP01	NRL N7 NN21	0.1432	0.0171
TP01	NRO N7 NN38	0.1432	0.0171
TP06	KJ744432.1 <i>Aname</i> sp. MYG368 voucher T102108	0.1432	0.0171
TP06	NBL N26 AD658	0.1432	0.0171
TP01	OY25 NDW H-N57	0.1433	0.0135
TP01	PO20 NAG H-N113	0.1433	0.0135
TP01	PO28 NAG H-N113	0.1433	0.0135
TP01	RB07 H-N157	0.1433	0.0135
TP01	RB20	0.1433	0.0135
TP03	OY06 NRU H-N146	0.1433	0.0135
TP01	RB19	0.1435	0.0171
TP01	MN635068.1:305-631 <i>Aname watsoni</i> voucher WAMT104786	0.1437	0.0194
TP01	MN635069.1:305-631 <i>Aname watsoni</i> voucher WAMT104788	0.1437	0.0194
TP01	MN635071.1:305-631 <i>Aname watsoni</i> voucher WAMT104795	0.1437	0.0194
TP06	MN635068.1:305-631 <i>Aname watsoni</i> voucher WAMT104786	0.1437	0.0194
TP01	SY15 NTF <i>Aname watsoni</i>	0.1441	0.0134
TP01	SY16 NTF <i>Aname watsoni</i>	0.1441	0.0134
TP01	SY18 NTF <i>Aname watsoni</i>	0.1441	0.0134

Project specimen	Reference Specimen	P-Distance	Std. Err
TP01	SY24 NTF <i>Aname watsoni</i>	0.1441	0.0134
TP01	TM01	0.1441	0.0134
TP01	TM07	0.1441	0.0134
TP01	TM09	0.1441	0.0134
TP01	TM25	0.1441	0.0134
TP01	TM28	0.1441	0.0134
TP03	TS08	0.1441	0.0134
TP06	SS07 <i>Aname</i> sp. H-N190	0.1441	0.0134
TP06	TM39	0.1441	0.0134
TP03	MN433245.1 <i>Aname mellosa</i> isolate OV43	0.1441	0.0136
TP06	MN433240.1 <i>Aname mellosa</i> isolate OV30	0.1441	0.0136
TP06	MN433243.1 <i>Aname mellosa</i> isolate OV38	0.1441	0.0136
TP06	MN433248.1 <i>Aname mellosa</i> isolate OV53	0.1441	0.0136
TP06	MN433253.1 <i>Aname mellosa</i> isolate OV63	0.1441	0.0136
TP06	MN433254.1 <i>Aname mellosa</i> isolate OV65	0.1441	0.0136
TP01	MN635084.1 <i>Aname vernonorum</i> voucher WAMT98772	0.1444	0.0137
TP03	KJ744409.1 <i>Aname</i> sp. MYG001 T102040	0.1444	0.0137
TP06	KJ745327.1 <i>Aname mellosa</i> voucher T88699	0.1444	0.0137
TP06	KJ745339.1 <i>Aname mellosa</i> voucher T88713	0.1444	0.0137
TP01	KJ744646.1 <i>Aname</i> sp. MYG372 voucher T107003	0.1444	0.0138
TP01	MW518630.1 <i>Aname</i> sp. MYG578 isolate WAMT89030	0.1444	0.0138
TP06	JQ772133.1 <i>Aname</i> sp. 4 MGR-2012 voucher WAM:T96140	0.1444	0.0139
TP01	SB23	0.1445	0.0134
TP01	MW518671.1 <i>Aname</i> sp. MYG623 isolate WAMT144405	0.1446	0.0173
TP01	KJ744663.1 <i>Aname mellosa</i> voucher T107947	0.1446	0.0137
TP01	KJ744671.1 <i>Aname mellosa</i> voucher T107976	0.1446	0.0137
TP01	KJ744781.1 <i>Aname mellosa</i> T113636	0.1446	0.0137
TP01	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1446	0.0137
TP01	KJ745052.1 <i>Aname mellosa</i> voucher T122824	0.1446	0.0137
TP01	KJ745146.1 <i>Aname mellosa</i> voucher T126262	0.1446	0.0137
TP01	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.1446	0.0137
TP01	KJ745280.1 <i>Stanwellia</i> sp. MYG360 voucher T78539	0.1446	0.0137
TP01	KJ745365.1 <i>Aname mellosa</i> T92127	0.1446	0.0137
TP03	KJ744481.1 <i>Aname mellosa</i> voucher T102865	0.1446	0.0137
TP01	NAZ N6 AD457 <i>Aname sinuata</i> WAMT88604	0.1447	0.0177
TP03	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1447	0.0151
TP06	OY06 NRU H-N146	0.1448	0.0136
TP01	TM39	0.1456	0.0135
TP01	TS08	0.1456	0.0135
TP03	TM12	0.1456	0.0135
TP03	TM14	0.1456	0.0135
TP03	TM17	0.1456	0.0135
TP06	TS08	0.1456	0.0135
TP01	KJ744432.1 <i>Aname</i> sp. MYG368 voucher T102108	0.1456	0.0172
TP01	KJ744649.1 <i>Aname</i> sp. MYG373 T107089	0.1456	0.0172
TP01	KJ745239.1 <i>Aname</i> sp. MYG177 T74755	0.1456	0.0172
TP01	KJ745241.1	0.1456	0.0172
TP01	KJ745243.1	0.1456	0.0172
TP01	KJ745246.1	0.1456	0.0172
TP01	KJ745247.1	0.1456	0.0172
TP01	KJ745248.1	0.1456	0.0172
TP01	KJ745296.1 <i>Aname</i> sp. MYG364 T85262	0.1456	0.0172
TP01	NBL N26 AD658	0.1456	0.0172
TP01	NCO N88 O165	0.1456	0.0172

Project specimen	Reference Specimen	P-Distance	Std. Err
TP01	NCT N89 O190	0.1456	0.0172
TP01	NEP N16 AD253	0.1456	0.0172
TP01	NRM N7 NN37	0.1456	0.0172
TP01	QP59 H-N159	0.1456	0.0172
TP03	KJ744432.1 <i>Aname</i> sp. MYG368 voucher T102108	0.1456	0.0172
TP03	KJ744577.1 <i>Aname mellosa</i> T103913	0.1456	0.0172
TP03	KJ744651.1 <i>Aname mellosa</i> T107182	0.1456	0.0172
TP03	KJ745299.1 <i>Aname</i> sp. MYG001 T86678	0.1456	0.0172
TP03	NBL N26 AD658	0.1456	0.0172
TP03	NDD N101 O292	0.1456	0.0172
TP03	NEK N116 AD306	0.1456	0.0172
TP03	MN433247.1:1-679 <i>Aname mellosa</i> isolate OV48	0.1456	0.0137
TP06	MN433245.1 <i>Aname mellosa</i> isolate OV43	0.1456	0.0137
TP01	KJ744987.1 <i>Aname mellosa</i> T122215	0.1459	0.0138
TP03	KJ744462.1 <i>Aname mellosa</i> voucher T102746	0.1459	0.0138
TP03	KJ744650.1 <i>Aname mellosa</i> voucher T107181	0.1459	0.0138
TP03	MW518629.1 <i>Aname mellosa</i> isolate WAMT88665	0.1459	0.0138
TP06	KJ744409.1 <i>Aname</i> sp. MYG001 T102040	0.1459	0.0138
TP01	KJ744647.1 <i>Aname</i> sp. MYG372 voucher T107004	0.1459	0.0138
TP01	JQ772133.1 <i>Aname</i> sp. 4 MGR-2012 voucher WAM:T96140	0.1460	0.0139
TP01	SB37	0.1460	0.0135
TP03	SB37	0.1460	0.0135
TP01	KJ744505.1 <i>Aname mellosa</i> voucher T103199	0.1461	0.0138
TP01	KJ744540.1 <i>Aname mellosa</i> voucher T103239	0.1461	0.0138
TP01	KJ744630.1 <i>Aname mellosa</i> T105886	0.1461	0.0138
TP01	KJ744922.1 <i>Aname mellosa</i> voucher T119700	0.1461	0.0138
TP01	KJ744926.1 <i>Aname mellosa</i> voucher T119710	0.1461	0.0138
TP01	KJ745093.1 <i>Aname mellosa</i> T122870	0.1461	0.0138
TP01	KJ745159.1 <i>Aname mellosa</i> voucher T126279	0.1461	0.0138
TP03	KJ744473.1 <i>Aname mellosa</i> voucher T102833	0.1461	0.0138
TP03	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1461	0.0138
TP03	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.1461	0.0138
TP06	KJ744481.1 <i>Aname mellosa</i> voucher T102865	0.1461	0.0138
TP01	RB01 <i>Aname</i> sp N157	0.1463	0.0137
TP01	RB04 H-N157	0.1463	0.0137
TP01	RB05 N-N157	0.1463	0.0137
TP01	RB10 H-N157	0.1463	0.0137
TP01	RB49	0.1463	0.0137
TP06	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1465	0.0151
TP03	MN635069.1 <i>Aname watsoni</i> voucher WAMT104788	0.1468	0.0196
TP03	MN635071.1 <i>Aname watsoni</i> voucher WAMT104795	0.1468	0.0196
TP01	TS53	0.1470	0.0135
TP03	SV38	0.1470	0.0135
TP03	TM04	0.1470	0.0135
TP03	TM16	0.1470	0.0135
TP03	TM27	0.1470	0.0135
TP06	TM12	0.1470	0.0135
TP06	TM14	0.1470	0.0135
TP06	TM17	0.1470	0.0135
TP03	MN433250.1 <i>Aname mellosa</i> isolate OV57	0.1471	0.0137
TP06	MN433247.1 <i>Aname mellosa</i> isolate OV48	0.1471	0.0137
TP03	SY23 <i>Aname mellosa</i>	0.1472	0.0135
TP03	JQ772153.1 <i>Aname</i> sp. 3 MGR-2012 voucher WAM:T98434	0.1473	0.0174
TP03	JQ772155.1 <i>Aname</i> sp. 3 MGR-2012 voucher WAM:T98436	0.1473	0.0174

Project specimen	Reference Specimen	P-Distance	Std. Err
TP03	KJ744447.1 <i>Aname mellosa</i> voucher T102731	0.1474	0.0138
TP03	KJ744609.1	0.1474	0.0138
TP03	KJ744718.1 <i>Aname</i> sp. MYG00 T110197	0.1474	0.0138
TP03	MH932613.1 <i>Aname mellosa</i> voucher WAMT146058	0.1474	0.0138
TP06	KJ744462.1 <i>Aname mellosa</i> voucher T102746	0.1474	0.0138
TP06	KJ744650.1 <i>Aname mellosa</i> voucher T107181	0.1474	0.0138
TP06	MW518629.1 <i>Aname mellosa</i> isolate WAMT88665	0.1474	0.0138
TP01	SB25	0.1474	0.0135
TP01	SB27	0.1474	0.0135
TP01	SB32	0.1474	0.0135
TP01	SB38	0.1474	0.0135
TP06	SB37	0.1474	0.0135
TP01	KJ744394.1 <i>Aname mellosa</i> T101158	0.1476	0.0138
TP01	KJ744923.1 <i>Aname mellosa</i> voucher T119702	0.1476	0.0138
TP01	KJ744977.1 <i>Aname mellosa</i> voucher T122200	0.1476	0.0138
TP01	KJ745051.1 <i>Aname mellosa</i> T122823	0.1476	0.0138
TP03	KJ744480.1 <i>Aname mellosa</i> voucher T102860	0.1476	0.0138
TP03	KJ744505.1 <i>Aname mellosa</i> voucher T103199	0.1476	0.0138
TP03	KJ744694.1 <i>Aname mellosa</i> voucher T109118	0.1476	0.0138
TP03	KJ745466.1 <i>Aname mellosa</i> voucher T98764	0.1476	0.0138
TP03	KJ745476.1 <i>Aname mellosa</i> voucher T98867	0.1476	0.0138
TP03	KJ745496.1 <i>Aname mellosa</i> voucher T99585	0.1476	0.0138
TP06	KJ744473.1 <i>Aname mellosa</i> voucher T102833	0.1476	0.0138
TP06	KJ744803.1 <i>Aname mellosa</i> voucher T113666	0.1476	0.0138
TP06	KJ745155.1 <i>Aname mellosa</i> voucher T126273	0.1476	0.0138
TP06	KJ745280.1 <i>Stanwellia</i> sp. MYG360 voucher T78539	0.1476	0.0138
TP03	JQ772146.1	0.1477	0.0175
TP01	OU30 NCT H-N89	0.1478	0.0137
TP01	RB14 <i>Aname</i> sp. N157	0.1478	0.0137
TP03	QZ04	0.1478	0.0137
TP01	JQ772141.1 <i>Aname</i> sp. 2 MGR-2012 T98897	0.1480	0.0173
TP01	KJ745240.1	0.1480	0.0173
TP01	MG800146.1 <i>Aname</i> sp. MYG479 voucher WAMT56760	0.1480	0.0173
TP01	MG800161.1 <i>Aname</i> sp. MYG102 AMT 98767	0.1480	0.0173
TP01	MW518626.1 <i>Aname</i> sp. MYG276 isolate WAMT72372	0.1480	0.0173
TP01	NAQ N5 AD352	0.1480	0.0173
TP01	NGU N16 DW10	0.1480	0.0173
TP01	QP37 H-N159	0.1480	0.0173
TP01	T98767 <i>Aname</i> MYG102 NHI	0.1480	0.0173
TP03	KJ744571.1 <i>Aname mellosa</i> T103906	0.1480	0.0173
TP06	KJ744577.1 <i>Aname mellosa</i> T103913	0.1480	0.0173
TP06	KJ744651.1 <i>Aname mellosa</i> T107182	0.1480	0.0173
TP06	KJ745299.1 <i>Aname</i> sp. MYG001 T86678	0.1480	0.0173
TP06	NDD N101 O292	0.1480	0.0173
TP06	NDQ N99 O344	0.1480	0.0173
TP06	NEK N116 AD306	0.1480	0.0173
TP03	KJ744722.1 <i>Aname</i> sp. MYG001 T110203	0.1483	0.0139
TP01	SY28 <i>Aname mellosa</i>	0.1485	0.0136
TP03	SV39	0.1485	0.0136
TP03	TM02	0.1485	0.0136
TP03	TM03	0.1485	0.0136
TP03	TM24	0.1485	0.0136
TP03	TS53	0.1485	0.0136
TP06	SV38	0.1485	0.0136

Project specimen	Reference Specimen	P-Distance	Std. Err
TP06	TM04	0.1485	0.0136
TP06	TM16	0.1485	0.0136
TP06	TM27	0.1485	0.0136
TP03	MN433234.1 <i>Aname mellosa</i> isolate OV20	0.1486	0.0138
TP06	MN433250.1 <i>Aname mellosa</i> isolate OV57	0.1486	0.0138
TP01	MN635085.1 <i>Aname vernonorum</i> voucher WAMT98775	0.1487	0.0174
TP06	SY23 <i>Aname mellosa</i>	0.1487	0.0136
TP01	NCZ N110 O285	0.1489	0.0177
TP03	SB32	0.1489	0.0136
TP03	SB33	0.1489	0.0136
TP01	MN635086.1 <i>Aname vernonorum</i> voucher WAMT98777	0.1489	0.0139
TP03	KJ744645.1 <i>Aname mellosa</i> voucher T107001	0.1489	0.0139
TP03	KJ744721.1 <i>Aname</i> sp. MYG001 voucher T110202	0.1489	0.0139
TP03	KJ744724.1 <i>Aname</i> sp. MYG001 T110206	0.1489	0.0139
TP03	KJ745328.1 <i>Aname mellosa</i> voucher T88700	0.1489	0.0139
TP03	KJ745331.1 <i>Aname mellosa</i> voucher T88703	0.1489	0.0139
TP03	MW518657.1 <i>Aname</i> sp. MYG212 isolate WAMT130488	0.1489	0.0139
TP06	KJ744447.1 <i>Aname mellosa</i> voucher T102731	0.1489	0.0139
TP06	KJ744609.1	0.1489	0.0139
TP06	KJ744718.1 <i>Aname</i> sp. MYG00 T110197	0.1489	0.0139
TP06	MH932613.1 <i>Aname mellosa</i> voucher WAMT146058	0.1489	0.0139
TP01	KJ744688.1 <i>Aname</i> sp. MYG214 voucher T108978	0.1492	0.0139
TP01	KJ744890.1 <i>Aname mellosa</i> voucher T116858	0.1492	0.0139
TP01	KJ745065.1 <i>Aname mellosa</i> voucher T122839	0.1492	0.0139
TP01	KJ745184.1 <i>Aname mellosa</i> voucher T127219	0.1492	0.0139
TP01	MW518665.1 <i>Aname</i> sp. MYG223 isolate WAMT132369	0.1492	0.0139
TP03	KJ744663.1 <i>Aname mellosa</i> voucher T107947	0.1492	0.0139
TP03	KJ744671.1 <i>Aname mellosa</i> voucher T107976	0.1492	0.0139
TP03	KJ744989.1 <i>Aname mellosa</i> voucher T122218	0.1492	0.0139
TP03	KJ745184.1 <i>Aname mellosa</i> voucher T127219	0.1492	0.0139
TP03	KJ745280.1 <i>Stanwellia</i> sp. MYG360 voucher T78539	0.1492	0.0139
TP06	KJ744480.1 <i>Aname mellosa</i> voucher T102860	0.1492	0.0139
TP06	KJ744505.1 <i>Aname mellosa</i> voucher T103199	0.1492	0.0139
TP06	KJ744694.1 <i>Aname mellosa</i> voucher T109118	0.1492	0.0139
TP06	KJ745466.1 <i>Aname mellosa</i> voucher T98764	0.1492	0.0139
TP06	KJ745476.1 <i>Aname mellosa</i> voucher T98867	0.1492	0.0139
TP06	KJ745496.1 <i>Aname mellosa</i> voucher T99585	0.1492	0.0139
TP01	QZ05	0.1493	0.0138
TP01	RB02 H-N158	0.1493	0.0138
TP01	RB12 <i>Aname</i> sp. H-N84	0.1493	0.0138
TP01	RB15 <i>Aname</i> sp. H-N84	0.1493	0.0138
TP03	RB14 <i>Aname</i> sp. N157	0.1493	0.0138
TP06	QZ04	0.1493	0.0138

Table A2. 2: Genetic p-distance and the associated standard error from reference specimens showing less than 15% sequence divergence from the *Kwonkan* specimens TP02/TP05 (Molecular ID: *Kwonkan* sp. H-N197).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP02	TP05	0.0000	0.0000
TP02	SV41 <i>Kwonkan</i> H-N197	0.0597	0.0090
TP02	SV40 <i>Kwonkan</i> H-N197	0.0611	0.0091
TP02	SV46 <i>Kwonkan</i> H-N197	0.0611	0.0091
TP02	SV47 <i>Kwonkan</i> H-N197	0.0626	0.0092
TP02	SV48 <i>Kwonkan</i> H-N197	0.0626	0.0092
TP02	SV25 <i>Kwonkan</i> H-N197	0.0640	0.0093
TP02	SS09 <i>Kwonkan</i> H-N191	0.1157	0.0154
TP02	SV04 <i>Kwonkan</i> H-N196	0.1237	0.0126
TP02	SY27 NTD <i>Kwonkan</i> H-N202	0.1266	0.0127
TP02	KJ744975.1 <i>Aname</i> sp. MYG250 voucher T121597	0.1289	0.0164
TP02	NRW N144 OU21	0.1289	0.0164
TP02	OU21 NRW <i>Kwonkan</i> H-N144	0.1289	0.0164
TP02	T121597 <i>Aname</i> MYG250 NHQ	0.1289	0.0164
TP02	SY14 NTB <i>Kwonkan</i> H-N201	0.1310	0.0129
TP02	SY19 NTB <i>Kwonkan</i> H-N201	0.1310	0.0129
TP02	SY25 NTB <i>Kwonkan</i> H-N201	0.1310	0.0129
TP02	NK N36 AD110	0.1313	0.0165
TP02	T101209 <i>Kwonkan</i> MYG175 NHP	0.1313	0.0165
TP02	SB31 <i>Kwonkan</i> H-N134	0.1314	0.0129
TP02	SB29 <i>Kwonkan</i> H-N134	0.1353	0.0143
TP02	TM15 <i>Kwonkan</i> MYG336	0.1354	0.0131
TP02	SJ02 <i>Aname</i> H-N187	0.1368	0.0131
TP02	SV26 <i>Kwonkan</i> H-N168	0.1383	0.0132
TP02	RB26 H-N159	0.1388	0.0134
TP02	RV06 <i>Kwonkan</i> H-N168	0.1401	0.0133
TP02	NAB N46 AS41	0.1408	0.0170
TP02	NFO N127 CB26	0.1408	0.0170
TP02	KJ745117.1	0.1411	0.0170
TP02	KJ745210.1	0.1411	0.0170
TP02	SV02 <i>Kwonkan</i> H-N130	0.1412	0.0133
TP02	SV28 <i>Kwonkan</i> H-N168	0.1412	0.0133
TP02	SY26 NTC <i>Kwonkan</i> H-N201	0.1412	0.0133
TP02	NAA N45 AS38	0.1422	0.0171
TP02	RV04 <i>Kwonkan</i> H-N168	0.1431	0.0134
TP02	NDK N94 O333	0.1432	0.0171
TP02	NCG N95 I16	0.1449	0.0173
TP02	NGQ N134 DG3	0.1450	0.0176
TP02	SV27 <i>Kwonkan</i> H-N168	0.1450	0.0137
TP02	MG800176.1 <i>Kwonkan</i> sp. MYG394 voucher WAMT132366	0.1451	0.0138
TP02	NGE N130 CW14	0.1458	0.0178
TP02	NRC PC15 N150	0.1459	0.0173
TP02	RB30 H-N160	0.1463	0.0137
TP02	NRZ PC18 N147	0.1480	0.0173
TP02	SV43 <i>Kwonkan</i> H-N199	0.1485	0.0136
TP02	SY10 NTA <i>Kwonkan</i> H-N200	0.1485	0.0136
TP02	TS52	0.1485	0.0136
TP02	PC18 NRZ H-N147	0.1488	0.0142
TP02	SR01 <i>Kwonkan</i> H-N188	0.1489	0.0136

Table A2. 3: Genetic p-distance and the associated standard error from reference specimens showing less than 15% sequence divergence from the Halonoproctidae specimen TP08 (Molecular ID: *Conothele* sp. H-C29).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP08	SV56 <i>Conothele</i> H-C29	0.0703	0.0122
TP08	SV61 <i>Conothele</i> H-C29	0.0703	0.0122
TP08	SV58 <i>Conothele</i> H-C29	0.0759	0.0127
TP08	SV57 <i>Conothele</i> H-C29	0.0782	0.0129
TP08	SV60 <i>Conothele</i> H-C29	0.0805	0.0130
TP08	OY10 H-C27 voucher T148197	0.0911	0.0137
TP08	CF C11 AN39	0.0998	0.0143
TP08	CAO H-C27 OO05	0.1032	0.0146
TP08	OO05 <i>Conothele</i> H-C27	0.1032	0.0146
TP08	MK735588.1 <i>Conothele</i> sp. MYG087 voucher WAMT99684	0.1033	0.0147
TP08	KJ744763.1 <i>Conothele</i> sp. MYG279 voucher T113615	0.1035	0.0148
TP08	OY14 <i>Conothele</i> H-C27 voucher T148201	0.1048	0.0146
TP08	CAG H-C11 BV016	0.1066	0.0147
TP08	CG H-C13 AT1	0.1078	0.0149
TP08	CJ C11 AD313 H-C11 voucher T107187	0.1078	0.0149
TP08	KJ744653.1 <i>Conothele</i> sp. MYG279 voucher T107187	0.1090	0.0152
TP08	KJ744950.1 <i>Conothele</i> sp. MYG279 voucher T119982	0.1090	0.0152
TP08	KJ744984.1 <i>Conothele</i> sp. MYG279 voucher T122211	0.1106	0.0152
TP08	SV54 <i>Conothele</i> MYG541	0.1111	0.0150
TP08	SV63 <i>Conothele</i> MYG541	0.1111	0.0150
TP08	MK735590.1 <i>Conothele</i> sp. MYG542 voucher WAMT101974	0.1129	0.0154
TP08	MK735595.1 <i>Conothele</i> sp. MYG542 voucher WAMT101982	0.1129	0.0154
TP08	MK735596.1 <i>Conothele</i> sp. MYG542 voucher WAMT101983	0.1129	0.0154
TP08	MK735597.1 <i>Conothele</i> sp. MYG542 voucher WAMT101984	0.1129	0.0154
TP08	MK735600.1 <i>Conothele</i> sp. MYG542 voucher WAMT101992	0.1129	0.0154
TP08	MK735618.1 <i>Conothele</i> sp. MYG541 voucher WAMT125186	0.1129	0.0154
TP08	CAN H-C26 OO06	0.1139	0.0152
TP08	CAO H-C11 HX1	0.1152	0.0153
TP08	MK735606.1 <i>Conothele</i> sp. MYG540 voucher WAMT110360	0.1153	0.0155
TP08	MK735621.1 <i>Conothele</i> sp. MYG537 voucher WAMT131212	0.1153	0.0155
TP08	Cnew C12 GZ21	0.1159	0.0153
TP08	CAH H-C23 BV033	0.1161	0.0156
TP08	MK735591.1 <i>Conothele</i> sp. MYG542 voucher WAMT101977	0.1176	0.0156
TP08	MK735598.1 <i>Conothele</i> sp. MYG542 voucher WAMT101988	0.1176	0.0156
TP08	MK735599.1 <i>Conothele</i> sp. MYG542 voucher WAMT101990	0.1176	0.0156
TP08	CAM H-C11 DW8	0.1179	0.0154
TP08	CP C12 AD711	0.1190	0.0155
TP08	MK735589.1 <i>Conothele</i> sp. MYG542 voucher WAMT101973	0.1200	0.0158
TP08	MW078436.1 <i>Conothele</i> sp. MYG716 voucher WAMT151329	0.1203	0.0158
TP08	CZ H-C20 AD530	0.1213	0.0156
TP08	KJ744485.1 <i>Conothele</i> sp. MYG279 voucher T102887	0.1224	0.0159
TP08	MK735593.1 <i>Conothele</i> sp. MYG542 voucher WAMT101979	0.1224	0.0159
TP08	MK735594.1 <i>Conothele</i> sp. MYG542 voucher WAMT101980	0.1224	0.0159
TP08	CN H-C16 AD635	0.1227	0.0156
TP08	CH H-C13 AT3	0.1239	0.0158
TP08	CO C14 AD326	0.1239	0.0158
TP08	MK735582.1 <i>Conothele</i> sp. MYG560 voucher WAMT89034	0.1244	0.0160
TP08	MK735592.1 <i>Conothele</i> sp. MYG542 voucher WAMT101978	0.1247	0.0160
TP08	MK735646.1 <i>Conothele</i> sp. MYG558 voucher WAMT136806	0.1247	0.0160
TP08	KJ744674.1 <i>Conothele</i> sp. MYG294 voucher T107984	0.1271	0.0162
TP08	KJ744966.1 <i>Conothele</i> sp. MYG279 voucher T120005	0.1271	0.0162
TP08	KJ745367.1 <i>Conothele</i> sp. MYG297 voucher T92159	0.1271	0.0162
TP08	MK735615.1 <i>Conothele</i> sp. MYG537 voucher WAMT122090	0.1271	0.0162

Project specimen	Reference Specimen	P-Distance	Std. Err
TP08	MK735623.1 <i>Conothele</i> sp. MYG537 voucher WAMT131214	0.1294	0.0163
TP08	MK735620.1 <i>Conothele</i> sp. MYG297 voucher WAMT127743	0.1316	0.0165
TP08	MK735617.1 <i>Conothele</i> sp. MYG538 voucher WAMT122092	0.1341	0.0165
TP08	MK735622.1 <i>Conothele</i> sp. MYG538 voucher WAMT131213	0.1341	0.0165
TP08	MK735605.1 <i>Conothele</i> sp. MYG297 voucher WAMT110214	0.1365	0.0167
TP08	MK735578.1 <i>Conothele</i> sp. MYG532 voucher WAMT55990	0.1385	0.0167
TP08	MK735604.1 <i>Conothele</i> sp. MYG297 voucher WAMT107722	0.1388	0.0168
TP08	MK735613.1 <i>Conothele</i> sp. MYG539 voucher WAMT120025 c	0.1398	0.0169
TP08	MK735616.1 <i>Conothele</i> sp. MYG538 voucher WAMT122091	0.1412	0.0169
TP08	MK735634.1 <i>Conothele</i> sp. MYG559 voucher WAMT135059	0.1450	0.0176
TP08	QP08	0.1451	0.0168
TP08	MK735577.1 <i>Conothele</i> sp. MYG532 voucher WAMT55988	0.1455	0.0171
TP08	MN433221.1 <i>Conothele</i> sp. OV02	0.1458	0.0168
TP08	SY20 <i>Conothele</i> sp. MYG528	0.1474	0.0169
TP08	MK735581.1 <i>Conothele</i> sp. MYG059 voucher WAMT81279	0.1479	0.0172
TP08	MK735665.1 <i>Conothele</i> sp. MYG550 voucher WAMT140753	0.1479	0.0172

Table A2. 4: Genetic p-distance and the associated standard error from reference specimens showing less than 15% sequence divergence from the COI sequenced Idiopidae specimens TP07 (Molecular ID: *Idiosoma* sp. H-I90) and TP09 (Molecular ID: *Idiosoma* sp. H-I91).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP09	BV011 IBM H-I57	0.1139	0.0152
TP09	AT15 IE H-I9 voucher T119983	0.1170	0.0154
TP09	KJ744981.1 <i>Aganippe</i> sp. MYG300 voucher T122206	0.1174	0.0156
TP09	CB40 ICA H-I57	0.1189	0.0156
TP09	KJ744951.1 <i>Aganippe</i> sp. MYG300 voucher T119983	0.1197	0.0157
TP09	KJ745124.1 <i>Aganippe</i> sp. MYG300 voucher T125338	0.1197	0.0157
TP09	KY295330.1 <i>Aganippe</i> sp. WAM T131974	0.1214	0.0159
TP09	KJ744986.1 <i>Aganippe</i> sp. MYG300 voucher T122214	0.1244	0.0160
TP09	BV080 IBQ H-I59	0.1253	0.0158
TP09	SV69 <i>Idiosoma</i> H-I82	0.1264	0.0159
TP09	BW17 IBU	0.1268	0.0161
TP09	KY295333.1 <i>Aganippe</i> sp. SAM SH52 voucher SAM-SH52	0.1268	0.0161
TP07	SB06 <i>Idiosoma</i> MYG256/H-I65	0.1270	0.0127
TP07	SB07 <i>Idiosoma</i> MYG256/H-I65	0.1270	0.0127
TP07	SB11 <i>Idiosoma</i> MYG256/H-I65	0.1270	0.0127
TP07	SB13 <i>Idiosoma</i> MYG256/H-I65	0.1270	0.0127
TP07	SR13 <i>Idiosoma</i> MYG256/H-I65	0.1295	0.0128
TP07	SR19 <i>Idiosoma</i> MYG256/H-I65	0.1295	0.0128
TP07	SR20 <i>Idiosoma</i> MYG256/H-I65	0.1295	0.0128
TP07	SB19 <i>Idiosoma</i> MYG256/H-I65	0.1299	0.0128
TP09	BV035 IBN H-I58	0.1300	0.0164
TP09	SB17 <i>Idiosoma</i> MYG256/H-I65	0.1300	0.0164
TP09	CB13 IBW H-I60	0.1305	0.0163
TP09	SS10 <i>Idiosoma</i> sp. H-I87	0.1310	0.0162
TP07	SB17 <i>Idiosoma</i> MYG256/H-I65	0.1314	0.0129
TP09	KY295323 <i>Aganippe</i> sp. WAM T122088	0.1315	0.0164
TP07	KY295320.1 <i>Aganippe</i> sp. WAM T96408	0.1317	0.0132
TP07	KJ745099.1 <i>Aganippe</i> MYG256 voucher T123106	0.1322	0.0132
TP07	SR21 <i>Idiosoma</i> MYG256/H-I65	0.1325	0.0129
TP07	SR23 <i>Idiosoma</i> MYG256/H-I65	0.1325	0.0129
TP07	O4 IBD <i>Idiosoma sigillatum</i> nigrum-group H-I17 Voucher T46054	0.1325	0.0154
TP09	KY295336.1 <i>Aganippe</i> sp. SAM SH16 voucher SAM-SH16	0.1338	0.0165
TP07	SR17 <i>Idiosoma</i> MYG256/H-I65	0.1339	0.0130
TP07	BV091 IBR H-I58	0.1348	0.0166
TP09	CB51 ICB H-I57	0.1352	0.0165
TP07	SR25 <i>Idiosoma</i> MYG256/H-I65	0.1356	0.0131
TP09	KJ745129.1 <i>Aganippe</i> sp. MYG300 voucher T125346	0.1362	0.0166
TP09	BV091 IBR H-I58	0.1371	0.0167
TP09	CB29 IBX H-I58	0.1371	0.0167
TP07	ICW I65 CZ22 <i>Idiosoma</i> H-I65	0.1375	0.0133
TP07	BZ58 IBV H-I7	0.1376	0.0132
TP07	T96486 <i>Aganippe</i> MYG019	0.1376	0.0132
TP09	KY295332 <i>Aganippe</i> sp. WAMT132760	0.1381	0.0168
TP09	SV64 <i>Idiosoma</i> H-I82	0.1383	0.0164
TP09	SV68 <i>Idiosoma</i> H-I82	0.1383	0.0164
TP09	RV01 <i>Idiosoma</i> H-I82	0.1390	0.0165
TP07	BV035 IBN H-I58	0.1395	0.0168
TP07	BV035 IBX H-I58	0.1395	0.0168
TP07	MW621136.1 <i>Aganippe</i> MYG256 voucher WAMT139805	0.1402	0.0136
TP09	OK342110.1 <i>Idiosoma gutharuka</i> voucher WAMT155372	0.1412	0.0166
TP09	RV03 <i>Idiosoma</i> H-I82	0.1412	0.0166
TP09	SB18 <i>Idiosoma</i> MYG224/ H-I85	0.1412	0.0166
TP09	BI7 IBL <i>Idiosoma</i> H-I53	0.1415	0.0172

Project specimen	Reference Specimen	P-Distance	Std. Err
TP07	KY295336.1 <i>Aganippe</i> sp. SAM SH16 voucher SAM-SH16	0.1416	0.0136
TP09	ICW I65 CZ22 <i>Idiosoma</i> H-I65	0.1419	0.0167
TP09	AD217 IQ H-I7 voucher T103905	0.1422	0.0167
TP09	O15e IY <i>Idiosoma</i> H-I30 voucher T65443	0.1422	0.0167
TP07	AD217 IQ H-I7 voucher T103905	0.1426	0.0135
TP09	SR11 <i>Idiosoma</i> MYG224/ H-I85	0.1429	0.0167
TP09	SR12 <i>Idiosoma</i> MYG224/ H-I85	0.1429	0.0167
TP09	SR16 <i>Idiosoma</i> MYG224/ H-I85	0.1429	0.0167
TP09	SV62 <i>Idiosoma</i> H-I82	0.1429	0.0167
TP09	SV66 <i>Idiosoma</i> H-I82	0.1429	0.0167
TP09	KY295314.1 <i>Aganippe</i> sp. WAM T131975 voucher WAM-T131975	0.1432	0.0170
TP07	O3 IBB <i>Idiosoma sigillatum</i> nigrum-group H-I17 voucher T44179	0.1434	0.0158
TP07	AD564 IP H-I8 voucher T92451	0.1435	0.0135
TP09	BZ58 IBV H-I7	0.1435	0.0167
TP09	MT835390.1 <i>Idiosoma gutharuka</i> voucher WAMT150972	0.1435	0.0167
TP09	RV02 <i>Idiosoma</i> H-I82	0.1435	0.0167
TP09	SB04 <i>Idiosoma</i> MYG224/ H-I85	0.1435	0.0167
TP09	SB10 <i>Idiosoma</i> H-I84	0.1435	0.0167
TP09	PO09 H-I70	0.1435	0.0170
TP07	SV69 <i>Idiosoma</i> H-I82	0.1448	0.0169
TP09	SR19 <i>Idiosoma</i> MYG256/H-I65	0.1451	0.0168
TP09	SR20 <i>Idiosoma</i> MYG256/H-I65	0.1451	0.0168
TP09	SR25 <i>Idiosoma</i> MYG256/H-I65	0.1451	0.0168
TP09	SV67 <i>Idiosoma</i> H-I82	0.1451	0.0168
TP07	KY295330.1 <i>Aganippe</i> sp. WAM T131974	0.1452	0.0172
TP07	BW17 IBU	0.1455	0.0171
TP09	KJ745099.1 <i>Aganippe</i> MYG256 voucher T123106	0.1455	0.0171
TP09	KY295228.1 <i>Aganippe</i> sp. WAM T129362 voucher WAM-T129362	0.1455	0.0171
TP09	KY295320.1 <i>Aganippe</i> sp. WAM T96408 voucher WAM-T96408	0.1455	0.0171
TP09	KY295337.1 <i>Aganippe cupulifex</i> voucher WAM-T133995	0.1455	0.0171
TP09	SB06	0.1458	0.0168
TP09	SB07	0.1458	0.0168
TP09	SB11	0.1458	0.0168
TP09	SB12	0.1458	0.0168
TP09	SB13	0.1458	0.0168
TP09	SB16	0.1458	0.0168
TP09	SB17	0.1458	0.0168
TP09	SB20	0.1458	0.0168
TP07	KY295228.1 <i>Aganippe</i> sp. WAM T129362 voucher WAM-T129362	0.1461	0.0138
TP09	PO08	0.1461	0.0169
TP09	I1 IAJ	0.1462	0.0181
TP09	MW621135.1 <i>Aganippe</i> sp. kalgoorlie 1 voucher WAMT139804	0.1462	0.0172
TP07	BV011 IBM H-I57	0.1464	0.0136
TP07	T123102 <i>Idiosoma sigillatum</i>	0.1464	0.0136
TP07	T96270 IAN	0.1465	0.0171
TP09	CB12 IBY	0.1466	0.0172
TP07	O1 IAZ <i>Idiosoma jarrah</i> nigrum-group H-I18	0.1473	0.0161
TP09	SR17	0.1474	0.0169
TP09	TM11	0.1474	0.0169
TP09	MH144639.1 <i>Idiosoma schoknechtorum</i> isolate NCB 004 T140765	0.1479	0.0172
TP07	KJ744951.1 <i>Aganippe</i> sp. MYG300 voucher T119983	0.1480	0.0140
TP09	AD564 IP	0.1481	0.0170
TP09	AI15 ID	0.1481	0.0170
TP09	O21 IBA	0.1481	0.0170
TP09	SB05	0.1481	0.0170
TP09	SB08	0.1481	0.0170

Project specimen	Reference Specimen	P-Distance	Std. Err
TP09	SB30	0.1481	0.0170
TP09	T123102 <i>Idiosoma sigillatum</i>	0.1481	0.0170
TP09	MH144630.1 <i>Idiosoma formosum</i> isolate NCB 012 T139470 M ID MYG262	0.1482	0.0172
TP07	CB13 IBW H-I60	0.1486	0.0138
TP09	T77637 IAT	0.1488	0.0172
TP09	AC13 IAI	0.1489	0.0173
TP07	MH144632.1 <i>Idiosoma mcnamarai</i> isolate NCB 014 T139496	0.1492	0.0139
TP09	CB39 IBZ	0.1492	0.0172
TP07	AR110 IF H-I7 voucher T116804	0.1494	0.0175
TP09	SR13	0.1497	0.0170
TP09	SR21	0.1497	0.0170
TP09	SR23	0.1497	0.0170
TP07	SV64 <i>Idiosoma</i> H-I82	0.1499	0.0136
TP07	AT15 IE H-I9 voucher T119983	0.1501	0.0138
TP09	KY295322 <i>Idiosoma (Aganippe)</i> sp. WAM T101994	0.1502	0.0173
TP07	KY295322 <i>Idiosoma (Aganippe)</i> sp. WAM T101994	0.1656	0.0145

Table A2. 5 Genetic p-distance and the associated standard error from reference specimens showing less than 20% sequence divergence from the CYTB sequenced Idiopidae specimens TP07-CYTB (Molecular ID: *Idiosoma* sp. H-I90) and TP09-CYB (Molecular ID: *Idiosoma* sp. H-I91).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP09 CYTB	KY295443.1 <i>Aganippe</i> sp. WAM T101994	0.1603	0.0140
TP09 CYTB	SV70 <i>Idiosoma</i> H-I89	0.1731	0.0140
TP09 CYTB	SS10 CytB <i>Idiosoma</i> H-I87	0.1766	0.0142
TP07 CYTB	KY295396.1 <i>Aganippe</i> sp. WAM T110336	0.1793	0.0146
TP09 CYTB	KY295396.1 <i>Aganippe</i> sp. WAM T110336	0.1808	0.0147
TP09 CYTB	KY295440.1 <i>Aganippe</i> sp. WAM T112855	0.1808	0.0147
TP09 CYTB	KY295451.1 <i>Aganippe</i> sp. WAM T131974	0.1825	0.0149
TP09 CYTB	SV65 <i>Idiosoma</i> H-I88	0.1854	0.0144
TP09 CYTB	SV62 Idiopidae H-I82	0.1882	0.0145
TP09 CYTB	SV64 Idiopidae H-I82	0.1882	0.0145
TP09 CYTB	RV02 Cytb Idiopidae H-I82	0.1892	0.0146
TP09 CYTB	SV66 Idiopidae H-I82	0.1896	0.0145
TP09 CYTB	SV67 Idiopidae H-I82	0.1896	0.0145
TP07 CYTB	SR13 <i>Idiosoma</i> H-I65 MYG256	0.1905	0.0146
TP09 CYTB	RV01 Cytb Idiopidae H-I82	0.1905	0.0146
TP09 CYTB	SB17 CytB <i>Idiosoma</i> H-I65 MYG256	0.1916	0.0147
TP09 CYTB	RV03 Cytb Idiopidae H-I82	0.1919	0.0147
TP09 CYTB	SR19 <i>Idiosoma</i> H-I65 MYG256	0.1933	0.0147
TP09 CYTB	SR20 <i>Idiosoma</i> H-I65 MYG256	0.1933	0.0147
TP07 CYTB	SB06 CytB <i>Idiosoma</i> H-I65 MYG256	0.1944	0.0148
TP07 CYTB	SB19 CytB <i>Idiosoma</i> H-I65 MYG256	0.1944	0.0148
TP07 CYTB	SR21 <i>Idiosoma</i> H-I65 MYG256	0.1947	0.0148
TP07 CYTB	SR23 <i>Idiosoma</i> H-I65 MYG256	0.1947	0.0148
TP07 CYTB	KY295440.1 <i>Aganippe</i> sp. WAM T112855	0.1953	0.0151
TP07 CYTB	SB07 CytB <i>Idiosoma</i> H-I65 MYG256	0.1958	0.0148
TP07 CYTB	SB17 CytB <i>Idiosoma</i> H-I65 MYG256	0.1958	0.0148
TP09 CYTB	SR25 <i>Idiosoma</i> H-I65 MYG256	0.1961	0.0148
TP09 CYTB	SB06 CytB <i>Idiosoma</i> H-I65 MYG256	0.1972	0.0149
TP09 CYTB	SB07 CytB <i>Idiosoma</i> H-I65 MYG256	0.1972	0.0149
TP09 CYTB	SB11 CytB <i>Idiosoma</i> H-I65 MYG256	0.1972	0.0149
TP09 CYTB	SB13 CytB <i>Idiosoma</i> H-I65 MYG256	0.1972	0.0149
TP09 CYTB	SB19 CytB <i>Idiosoma</i> H-I65 MYG256	0.1972	0.0149
TP07 CYTB	SR25 <i>Idiosoma</i> H-I65 MYG256	0.1975	0.0148
TP09 CYTB	SR13 <i>Idiosoma</i> H-I65 MYG256	0.1975	0.0148
TP09 CYTB	SR21 <i>Idiosoma</i> H-I65 MYG256	0.1975	0.0148
TP09 CYTB	SR23 <i>Idiosoma</i> H-I65 MYG256	0.1975	0.0148
TP09 CYTB	SV69 Idiopidae H-I82	0.1978	0.0148
TP07 CYTB	SB11 CytB <i>Idiosoma</i> H-I65 MYG256	0.1986	0.0149
TP07 CYTB	SB13 CytB <i>Idiosoma</i> H-I65 MYG256	0.1986	0.0149
TP07 CYTB	SR19 <i>Idiosoma</i> H-I65 MYG256	0.1989	0.0149
TP07 CYTB	SR20 <i>Idiosoma</i> H-I65 MYG256	0.1989	0.0149
TP07 CYTB	SS10 CytB <i>Idiosoma</i> H-I87	0.2003	0.0149

Table A2. 6: Genetic p-distance and the associated standard error from reference specimens showing less than 15% sequence divergence from the COI sequenced Buthidae specimen TP11 (Molecular ID: *Lychas 'annulatus – complex'*).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP11	SV73 <i>Lychas annulatus</i> complex	0.0422	0.0077
TP11	PP028575.1 <i>Lychas</i> sp. Biologic-SCOR012 isolate BES14903 BMR06337	0.0974	0.0116
TP11	QP69 <i>Lychas</i> sp. H-30	0.0990	0.0114
TP11	QP68 <i>Lychas</i> sp. H-29	0.1019	0.0115
TP11	SY35 <i>Lychas</i> sp. SCO046	0.1019	0.0115
TP11	MW078434.1 <i>Lychas</i> sp. SCO046 voucher WAMT151336	0.1020	0.0118
TP11	SV71 <i>Lychas adonis</i>	0.1033	0.0116
TP11	SV72 <i>Lychas adonis</i>	0.1033	0.0116
TP11	RL14 <i>Lychas</i> H-SCB008	0.1053	0.0150
TP11	SY33 <i>Lychas</i> sp. SCO046	0.1063	0.0118
TP11	ON929012.1 <i>Lychas</i> sp. Biologic-SCOR008 isolate BES9132 BMR05610	0.1065	0.0120
TP11	SY34 <i>Lychas</i> sp. SCO046	0.1077	0.0118
TP11	SY37 <i>Lychas</i> sp. SCO046	0.1077	0.0118
TP11	TS56	0.1077	0.0118
TP11	OR653641.1 <i>Lychas</i> sp. SCO023 isolate BES14404 BMR05520	0.1081	0.0121
TP11	QW13 <i>Lychas</i> H-SCB008	0.1081	0.0154
TP11	QW79 <i>Lychas</i> H-SCB008	0.1085	0.0151
TP11	QW81 <i>Lychas</i> H-SCB008	0.1085	0.0151
TP11	SV75 <i>Lychas</i> H-SCB005	0.1085	0.0149
TP11	SV76 <i>Lychas</i> H-SCB005	0.1085	0.0149
TP11	QW76 <i>Lychas</i> H-SCB010	0.1092	0.0119
TP11	QW77 <i>Lychas</i> H-SCB010	0.1092	0.0119
TP11	SY40 <i>Lychas</i> sp. SCO046	0.1092	0.0119
TP11	QW10 <i>Lychas</i> H-SCB008	0.1106	0.0152
TP11	QW11 <i>Lychas</i> H-SCB008	0.1106	0.0152
TP11	QW15 <i>Lychas</i> H-SCB008	0.1106	0.0152
TP11	SY38 <i>Lychas</i> H-SCB006	0.1106	0.0120
TP11	QW14 <i>Lychas</i> H-SCB008	0.1108	0.0152
TP11	QW80 <i>Lychas</i> H-SCB008	0.1108	0.0152
TP11	SV77 <i>Lychas</i> H-SCB005	0.1109	0.0151
TP11	OR653822.1 <i>Lychas</i> sp. Biologic-SCOR012 isolate BES4461 BMR06118	0.1109	0.0122
TP11	OR653586.1 <i>Lychas</i> sp. SCO024 isolate ABDA01 BMR04885	0.1111	0.0123
TP11	OR653584.1 <i>Lychas</i> sp. SCO024 isolate ABHH01 BMR04883	0.1113	0.0123
TP11	SC16 <i>Lychas</i> H-SCB008	0.1119	0.0151
TP11	OR653655.1 <i>Isometroides</i> sp. Biologic-SCOR010 isolate BES13873 BMR05688	0.1125	0.0123
TP11	OR653585.1 <i>Lychas</i> sp. SCO024 isolate ABHS01 BMR04884	0.1126	0.0123
TP11	QW12 <i>Lychas</i> H-SCB008	0.1132	0.0154
TP11	QP66 <i>Lychas</i> sp. H-27	0.1135	0.0121
TP11	TS55	0.1135	0.0121
TP11	TS57	0.1135	0.0121
TP11	MW078435.1 <i>Lychas</i> sp. SCO024 voucher WAMT151334	0.1142	0.0124
TP11	MW558023.1 <i>Isometroides</i> sp. SCO051 voucher WAMT152480	0.1142	0.0124
TP11	ON923769.1 <i>Lychas</i> sp. WAM-SCO039 isolate BES9917 BMR01078	0.1142	0.0124
TP11	OR653715.1 <i>Lychas</i> sp. WAM-SCO039 isolate BES4570 BMR05823	0.1142	0.0124
TP11	OR653733.1 <i>Lychas</i> sp. WAM-SCO039 isolate BES4768 BMR05846	0.1142	0.0124
TP11	RL08 <i>Lychas</i> H-SCB008	0.1152	0.0122
TP11	OR653663.1 <i>Isometroides</i> sp. Biologic-SCOR010 isolate BES14153 BMR05698	0.1155	0.0125
TP11	RL17 <i>Lychas</i> H-SCB009	0.1157	0.0122
TP11	RL29 <i>Lychas</i> H-SCB008	0.1164	0.0122
TP11	SY41 <i>Lychas</i> H-SCB007	0.1164	0.0122
TP11	OR653814.1 <i>Isometroides</i> sp. Biologic-SCOR010 isolate BES4933 BMR06085	0.1170	0.0125
TP11	OR653832.1 <i>Lychas</i> sp. SCO024 isolate AAOK01 BMR06130	0.1172	0.0125

Project specimen	Reference Specimen	P-Distance	Std. Err
TP11	SC15 <i>Lychas</i> H-SCB009	0.1175	0.0123
TP11	SC17 <i>Lychas</i> H-SCB009	0.1175	0.0123
TP11	OR653726.1 <i>Isometroides</i> sp. Biologic-SCOR010 isolate BES4219 BMR05838	0.1185	0.0126
TP11	SC18 <i>Lychas</i> H-SCB009	0.1189	0.0124
TP11	ON923828.1 <i>Lychas</i> sp. Biologic-SCOR003 isolate ESV18:0178 WAMT146518	0.1202	0.0127
TP11	MW558022.1 <i>Lychas</i> sp. SCO039 voucher WAMT152490	0.1204	0.0127
TP11	TS35	0.1237	0.0126
TP11	MF422313.1 <i>Isometrus</i> sp. BNHS SC 143	0.1242	0.0128
TP11	MN436716.1 <i>Lychas</i> sp. Biologic-SCOR001 voucher BMR00043	0.1309	0.0132
TP11	ON929037.1 <i>Lychas</i> sp. Biologic-SCOR001 isolate BES7631 BMR01743	0.1309	0.0132
TP11	ON929035.1 <i>Lychas</i> sp. Biologic-SCOR001 isolate BES9665 BMR01741	0.1339	0.0133
TP11	ON929034.1 <i>Lychas</i> sp. Biologic-SCOR001 isolate BES9503 BMR01737	0.1355	0.0134
TP11	MF422321.1 <i>Lychas tricarinatus</i> voucher INHER-Scorpion-13	0.1364	0.0134
TP11	MN436720.1 <i>Lychas</i> sp. Biologic-SCOR001 voucher BMR00047	0.1370	0.0134
TP11	ON929036.1 <i>Lychas</i> sp. Biologic-SCOR001 isolate BES6594 BMR01742	0.1370	0.0134
TP11	PP028666.1 <i>Lychas</i> sp. Biologic-SCOR001 isolate BES11030 BMR04372	0.1370	0.0134
TP11	JN018153.1 <i>Lychas mucronatus</i>	0.1375	0.0133
TP11	JN018154.1 <i>Parabuthus laevifrons</i>	0.1377	0.0136
TP11	MF422319.1 <i>Lychas tricarinatus</i> voucher INHER-Scorpion-11	0.1379	0.0134
TP11	MF422320.1 <i>Lychas tricarinatus</i> voucher INHER-Scorpion-12	0.1379	0.0134
TP11	MN436722.1 <i>Lychas</i> sp. Biologic-SCOR001 voucher BMR00049	0.1382	0.0139
TP11	NC 072215.1 <i>Lychas mucronatus</i> voucher LMUCR20220826	0.1391	0.0132
TP11	MN436721.1 <i>Lychas</i> sp. Biologic-SCOR001 voucher BMR00048	0.1392	0.0139
TP11	MF422319.1 <i>Lychas tricarinatus</i>	0.1394	0.0135
TP11	ON923842.1 <i>Lychas</i> sp. Biologic-SCOR006 isolate ESV18:0183 WAMT155914	0.1400	0.0135
TP11	MN436719.1 <i>Lychas</i> sp. Biologic-SCOR001 voucher BMR00046	0.1405	0.0141
TP11	KT716037.1 <i>Lychas tricarinatus</i> voucher WILD-13-ARA-1256	0.1408	0.0138
TP11	ON923768.1 <i>Lychas</i> sp. Biologic-SCOR006 isolate BES9995 BMR01077	0.1416	0.0136
TP11	ON923830.1 <i>Lychas</i> sp. Biologic-SCOR006 isolate ESV18:0241 WAMT146523	0.1431	0.0137
TP11	EF122605.2 <i>Centruroides vittatus</i>	0.1440	0.0137
TP11	KY982184.1 <i>Centruroides schmidtii</i>	0.1441	0.0135
TP11	MF422327.1 <i>Lychas tricarinatus</i> voucher BNHS:SC 150	0.1442	0.0137
TP11	MF422329.1 <i>Lychas tricarinatus</i> voucher BNHS:SC 144	0.1442	0.0137
TP11	ON923829.1 <i>Lychas</i> sp. Biologic-SCOR006 isolate ESV18:0181 WAMT146521	0.1446	0.0137
TP11	KF997876.1 <i>Mesobuthus gibbosus</i>	0.1467	0.0137
TP11	ON923841.1 <i>Lychas</i> sp. Biologic-SCOR006 isolate ESV18:0196 WAMT155913	0.1479	0.0139
TP11	MF422323.1 <i>Lychas tricarinatus</i> voucher BNHS:SC 146	0.1500	0.0139

Table A2. 7: Genetic p-distance and the associated standard error from reference specimens showing less than 20% sequence divergence from the 16S sequenced Buthidae specimen TP11 16S (Molecular ID: *Lychas* sp. H-SCB011).

Project specimen	Reference Specimen	P-Distance	Std. Err
TP11 16S	OR802156.1 <i>Isometrus lithophilis</i> voucher IES-465 large subunit ribosomal RNA	0.1701	0.0203
TP11 16S	AF370855.1 <i>Lychas mucronatus</i> 16S ribosomal RNA gene	0.1746	0.0206
TP11 16S	NC 072215.1 <i>Lychas mucronatus</i> voucher LMUCR20220826	0.1756	0.0208
TP11 16S	ON262631.1 <i>Janalychas srilankensis</i> isolate S855 large subunit ribosomal RNA	0.1774	0.0217
TP11 16S	KY981921.1 <i>Isometrus maculatus</i> voucher AMCC LP-1798 16S ribosomal RNA gene	0.1813	0.0208
TP11 16S	ON262636.1 <i>Lychas scutillus</i> isolate B061 large subunit ribosomal RNA gene	0.1818	0.0220
TP11 16S	OK644013.1 <i>Isometrus tamhini</i> voucher INSC164 INHER342 large subunit ribosomal RNA	0.1837	0.0209
TP11 16S	OK644014.1 <i>Isometrus tamhini</i> voucher INSC006 BNHS SC 155 large subunit ribosomal RNA	0.1837	0.0209
TP11 16S	OK644022.1 <i>Isometrus</i> sp. 1 SSS-2021 INSC054 BNHS SC 190 large subunit ribosomal RNA	0.1866	0.0210
TP11 16S	OK644018.1 <i>Isometrus sankeriensis</i> voucher INSC121 INHER289 large subunit ribosomal RNA	0.1895	0.0212
TP11 16S	OK644019.1: <i>Isometrus thurstoni</i> voucher INSC041 INHER130 large subunit ribosomal RNA	0.1895	0.0212
TP11 16S	OK644021.1 <i>Isometrus</i> sp. 2 SSS-2021 voucher INSC117 INHER294 large subunit ribosomal RNA	0.1912	0.0213
TP11 16S	ON262658.1: <i>Reddyanus basilicus</i> isolate S880 large subunit ribosomal RNA	0.1929	0.0224
TP11 16S	OK644020.1 <i>Isometrus</i> sp. 2 SSS-2021 voucher INSC132 INHER276 large subunit ribosomal RNA	0.1941	0.0215
TP11 16S	OK644015.1 <i>Isometrus amboli</i> voucher INSC008 BNHS SC 157 large subunit ribosomal RNA	0.1953	0.0214
TP11 16S	OK644023.1 <i>Isometrus kovariki</i> voucher INSC040 BNHS SC 162 large subunit ribosomal RNA	0.1953	0.0214
TP11 16S	MK479024.1 <i>Centruroides hentzi</i> isolate 1673 16S ribosomal RNA	0.1988	0.0216
TP11 16S	MK479049.1 <i>Centruroides sissomi</i> isolate 7597 16S ribosomal RNA	0.1988	0.0216
TP11 16S	OR802157.1 <i>Isometrus adviteeya</i> voucher IES-419 large subunit ribosomal RNA	0.1994	0.0216



Appendix 2

Invertebrate Fauna Records

Specimen	Site	Group	Family	Species
M20240301.WIB02SRE_MG-01	WIB02SRE	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. H-N205
M20240301.WIB03SRE_MG-04	WIB03SRE	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. H-N206
M20240301.WIB03SRE_MG-02	WIB03SRE	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. H-N206
M20240301.WIB03SRE_MG-05	WIB03SRE	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. H-N206
M20170904.AHF13.SRE-01	AHF13PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N138
M20170829.AHF13.SRE-01	AHF13PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N138
M20170901.AHF.SRE03-01	AHFSRE03	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N139
M20170901.AHF.SRE03-02	AHFSRE03	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N139
M20170830.AHF.SRE02-02	AHFSRE02	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N140
M20190518.WINSRE07-03	WINSRE07	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N147
M20190924.WIN01P-01	WIN01P	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N148
M20190518.WINSRE07-01	WINSRE07	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N148
M20190513.WINSRE02-01	WINSRE02	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N149
M20190923.WIN09P-02	WIN09P	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N152
M20190923.WIN09P-01	WIN09P	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N152
M20190924.WIN09P-01	WIN09P	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N152
M20190923.WIN02P-01	WIN02P	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N153
M20170831.AHF01-01	AHF01PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170904.AHF01-01	AHF01PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170903.AHF06-01	AHF06PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170830.AHF07-01	AHF07PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7

Specimen	Site	Group	Family	Species
M20170830.AHF07-02	AHF07PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170903.AHF07-01	AHF07PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170830.AHF10-01	AHF10PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170904.AHF10.SRE-01	AHF10PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170904.AHF12.SRE-01	AHF13PF	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20170904.AHF???.Bary-02	AHFSRE01	Mygalomorph Spider	Anamidae	<i>Aname</i> sp. N7
M20190518.WINSRE06-03	WINSRE06	Mygalomorph Spider	Anamidae	Anamidae sp.
M20190518.WINSRE04-01	WINSRE04	Mygalomorph Spider	Anamidae	Genus? sp. N150
M20240301.WIB03SRE_MG-03	WIB03SRE	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. H-N197
M20240301.WIB03SRE_MG-01	WIB03SRE	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. H-N197
M20190513.WINSRE02-02	WINSRE02	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190517.WINSRE03-01	WINSRE03	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE03-01	WINSRE03	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190516.WINSRE05-01	WINSRE05	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190516.WINSRE05-02	WINSRE05	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE06-01	WINSRE06	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE06-02	WINSRE06	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE07-02	WINSRE07	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-01	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-02	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-03	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151

Specimen	Site	Group	Family	Species
M20190518.WINSRE08-04	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-05	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-06	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190518.WINSRE08-07	WINSRE08	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M20190921.WINSRE12-01	WINSRE12	Mygalomorph Spider	Anamidae	<i>Kwonkan</i> sp. N151
M2024513.WIB11SRE_MG-02	WIB11SRE	Mygalomorph Spider	Barychelidae	Barychelidae sp.
M20190520.WIN09P-01	WIN09P	Mygalomorph Spider	Barychelidae	<i>Idiommata</i> sp. B39
M2024513.WIB12SRE_MG-02	WIB12SRE	Mygalomorph Spider	Halonoproctidae	<i>Conothele</i> sp. H-C29
M2024513.WIB12SRE_MG-01	WIB12SRE	Mygalomorph Spider	Idiopidae	<i>Idiosoma</i> sp. H-I90
M2024513.WIB11SRE_MG-01	WIB11SRE	Mygalomorph Spider	Idiopidae	<i>Idiosoma</i> sp. H-I91
M20170828.AHF12-01	AHF12PF	Mygalomorph Spider	Undetermined	Mygalomorphae sp.
M20170902.AHF13-02	AHF13PF	Mygalomorph Spider	Undetermined	Mygalomorphae sp.
M20170902.AHF13-01	AHF13PF	Mygalomorph Spider	Undetermined	Mygalomorphae sp.
M20170903.AHF13-01	AHF13PF	Mygalomorph Spider	Undetermined	Mygalomorphae sp.
M20170830.AHF.SRE02-01	AHFSRE02	Mygalomorph Spider	Undetermined	Mygalomorphae sp.
S20190919.WIN05P-01	WIN05P	Scorpion	Buthidae	<i>Lychas adonis</i>
Sc20170828AHF19-3	AHF19PF	Scorpion	Buthidae	<i>Lychas</i> 'annulatus complex'
Sc20170828AHF19-1	AHF19PF	Scorpion	Buthidae	<i>Lychas</i> 'annulatus complex'
Sc20170828AHF19-1	AHF19PF	Scorpion	Buthidae	<i>Lychas</i> 'annulatus complex'
S20190519.WIN05P-01	WIN05P	Scorpion	Buthidae	<i>Lychas</i> 'annulatus complex'
S20190515.WIN10P-02	WIN10P	Scorpion	Buthidae	<i>Lychas</i> 'annulatus complex'

Specimen	Site	Group	Family	Species
Sc20170828AHF16-2	AHF16PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
Sc20170828AHF16-1	AHF16PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
SC20170828AHF18-1	AHF18PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
SC20170828AHF19-2	AHF19PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
Sc20170828AHF19-2	AHF19PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
Sc20170828AHF19-4	AHF19PF	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S20190919.WIN01P-01	WIN01P	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S20190518.WIN02P-01	WIN02P	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S20190919.WIN04P-01	WIN04P	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S20190517.WIN08P-01	WIN08P	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S2024511.WIB07SRE_MG-01	WIB07SRE	Scorpion	Buthidae	<i>Lychas 'annulatus complex'</i>
S20190919.WIN04P-02	WIN04P	Scorpion	Buthidae	<i>Lychas sp.</i>
S20190518.WINSRE02-01	WINSRE02	Scorpion	Urodacidae	<i>Urodacus 'yaschenkoi complex'</i>
S20190518.WINSRE02-02	WINSRE02	Scorpion	Urodacidae	<i>Urodacus 'yaschenkoi complex'</i>
S20190515.WIN10P-01	WIN10P	Scorpion	Urodacidae	<i>Urodacus sp. 'telfer'</i>
S20190516.WIN04P-01	WIN04P	Scorpion	Urodacidae	<i>Urodacus varians</i>
S20190922.WIN10P-01	WIN10P	Scorpion	Urodacinae	<i>Urodacus sp. 'telfer'</i>

